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Gln Gly Phe Lys Asp Asp Ser Ala Phe Asp Cys Glu Asp Asp Asp Asp	
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Pro Thr His Leu Ser Gln Gln Tyr Cys Asn Asn Ser Phe Asp Asn Ser	
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Gly Ser Leu Ile Gly Leu Asn Asn Leu Ser Ser Ser Gln Ile His Gln	
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Pro Leu His Ser Ser Val Asp Ala Lys Leu Glu Ala Ile Cys Lys Ser	
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Gly Lys Lys Val Thr Gly Leu Asp Gly Asp Ala Glu Lys Ser Ala Asn	
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Lys	Leu	Lys	Ser	Met	Asp	Phe	Glu	Thr	Pro	Tyr	Asn	Asn	Thr	Glu	Trp
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Ser Tyr Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala Gln
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ttt tgt ctc cgc ggc ggc gat gct aat ttc aat ttc cct aat aat cca 298
Phe Cys Leu Arg Gly Gly Asp Ala Asn Phe Asn Phe Pro Asn Asn Pro
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gaa gaa tcg ggt tta gta ccc gga tcc gag atc cga cca gag tct cct 442  
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115 120 125

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ttt ttg gat ttg ctt ccg atg aat ttc ggg ttt gat tcc ttc tcc gac 538  
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gac ttc tct ggc ttc tcc ggt ggt gat cga ttt aca gag att tta ccc 586  
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atc gaa gat tac gga gga gag agt tta tta gat gaa tct ttg att ctt 634  
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180 185 190

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Trp Asp Phe  
195

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ccgggaattt ctttcgtttc ggatccgaat ttgatgtgga tcatattcac acctatattt 803

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35 40 45

Ser Tyr Asp Thr Pro Glu Lys Ala Ala Arg Ala Phe Asp Ala Ala Gln  
50 55 60

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Glu	Gly	Ala	Met	Lys	Phe	Gly	Ala	His	Ile	Lys	Gly	Asn	Gly	His	Asn	
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 180 185 190  
 Asn Lys Val Glu Phe Val Gln Thr Leu Arg Arg Glu Ser Ala Ser Phe  
 195 200 205  
 Gly Arg Gly Ser Ser Lys Tyr Lys Gly Leu Ala Leu Gln Lys Cys Thr  
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 Gln Phe Lys Thr His Asp Gln Ile His Leu Phe Gln Asn Arg Gly Trp  
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 245 250 255  
 Met Lys Phe Gly Ala His Ile Lys Gly Asn Gly His Asn Asp Leu Glu  
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 Lys Gln Ser Ser Ile Phe Leu Pro Met Ala Thr Met Lys Pro Leu Lys  
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Pro	Phe	Ile	Lys	Ser	Pro	Ser	Asn	Asp	Ser	Ser	Ala	Phe	Ala	Phe	Ser	
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 Lys Lys Ser Ser Ser Arg Lys Arg Ser Ser Thr Val Ala Val Lys Leu  
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 may be A, T, C, G, other or unknown

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 <223> Xaa at amino acid position 90 is either a Serine  
 or not present

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Ser Trp Val Ala Glu Ile Arg His Pro Leu Leu Lys Arg Arg Ile Trp  
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cta ggg acg ttc gag acc gca gag gag gca gca aga gca tac gac gag 201  
Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu  
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gcc gcc gtt tta atg agc ggc cgc aac gcc aaa acc aac ttt ccc ctc 249  
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aac aac aac aac acc gga gaa act tcc gag ggc aaa acc gat att tca 297  
Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser  
65 70 75 80  
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85 90 95  
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115 120 125  
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Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val  
130 135 140  
gag cta ggt ccc gca agc tcc tcc caa gag act act agt aaa gct tca 537  
Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser  
145 150 155 160  
caa gac gct att ctt gct ccg acc act gaa gtt gaa att ggt ggc agc 585  
Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser  
165 170 175  
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180 185 190  
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Glu Glu Leu Leu Asn Thr Asn  
195  
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&lt;223&gt; G975

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<223> Xaa at amino acid position 90 is either a Serine  
or not present

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35 40 45Ala Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu  
50 55 60Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser  
65 70 75 80Ala Ser Ser Thr Met Ser Ser Ser Thr Xaa Ser Ser Ser Leu Ser Ser  
85 90 95Ile Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser  
100 105 110Leu Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp  
115 120 125Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val  
130 135 140Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser  
145 150 155 160Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser  
165 170 175Arg Glu Glu Val Leu Asp Glu Glu Glu Lys Val Ala Leu Gln Met Ile  
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195

&lt;210&gt; 29

&lt;211&gt; 966

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

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&lt;222&gt; (72)..(815)

&lt;223&gt; G976

G975: 28-195

&lt;220&gt;

<223> "n" at various positions throughout the sequence  
may be A, T, C, G, other or unknown

&lt;220&gt;

<223> Xaa at amino acid position 77 may be various or  
unknown

&lt;400&gt; 29

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Ile Ile Gln Ser Ser Thr Ser Ser Ser Val Thr Ile Val Pro Val Pro
      15              20              25

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Thr Cys Gly Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys
      30              35              40              45

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Arg Cys Arg Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys
      95              100              105

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Thr Thr Arg Val Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala
110              115              120              125

gcc gca tat gac gtg gcg gcg tta gct ctt aaa ggt gga gac act ctc 494
Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu
      130              135              140

ttg aac ttc ccg gat tcc ctg gga tct tac ccc att ccc ata tct tct 542
Leu Asn Phe Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Ile Ser Ser
      145              150              155

tcc gca gct cat atc aga tgc gct gca gct gcg gct gct gcg act agg 590
Ser Ala Ala His Ile Arg Cys Ala Ala Ala Ala Ala Ala Thr Arg
      160              165              170

ggt gcg gct gga gcg gcc gtg aag gta ggt caa aag aag gaa gat aaa 638
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Ile	Ser	Arg	Arg	Lys	Lys	Asn	Pro	Val	Tyr	Arg	Gly	Ile	Arg	Cys	Arg	
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Ser	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	Glu	Pro	Lys	Lys	Thr	Thr	Arg	
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Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Ile Ser Ser Ser Ala Ala  
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His Ile Arg Cys Ala Ala Ala Ala Ala Ala Thr Arg Gly Ala Ala  
 165 170 175

Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys Val Tyr Asp  
 180 185 190

Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu Glu Leu Leu  
 195 200 205

Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met Met Val Ala  
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 <223> G977

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 may be A, T, C, G, other or unknown

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 Gln Gln Arg Phe Arg Gly Val Arg Gln Arg His Trp Gly Ser Trp Val  
 5 10 15 20

tcc gaa att cgt cac cct ctc ttg aaa aca aga atc tgg cta ggg acg 153  
 Ser Glu Ile Arg His Pro Leu Leu Lys Thr Arg Ile Trp Leu Gly Thr  
 25 30 35

ttt gag aca gcg gag gat gca gca agg gcc tac gac gag gcg gct agg 201  
 Phe Glu Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Glu Ala Ala Arg  
 40 45 50

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Leu Met Cys Gly Pro Arg Ala Arg Thr Asn Phe Pro Tyr Asn Pro Asn
      55                      60                      65

gcc att cct act tcc tct tcc aag ctt cta tca gca act ctt acc gct 297
Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala Thr Leu Thr Ala
      70                      75                      80

aaa ctc cac aaa tgc tac atg gct tct ctt caa atg acc aag caa acg 345
Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met Thr Lys Gln Thr
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caa aca caa acg caa acg cag acc gca aga tca caa tcc gcg gac agt 393
Gln Thr Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln Ser Ala Asp Ser
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gac ggt gtg acg gct aac gaa agt cat ttg aac aga gga gta acg gag 441
Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg Gly Val Thr Glu
                      120                      125                      130

acg aca gag atc aag tgg gaa gat gga aat gcg aat atg caa cag aat 489
Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn Met Gln Gln Asn
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Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met Ile Glu Glu Leu
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ctt cac tac ggt tcc att gag ctt tgc tct gtt tta cca act cag acg 585
Leu His Tyr Gly Ser Ile Glu Leu Cys Ser Val Leu Pro Thr Gln Thr
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ctg tgagaaatgg ccttgctcgtt ttagcgtatt cttttcattt ttatttttgt 638
Leu

ttccacaaaa acggcgtcgt aagtgatgag agtagtagtg agagaaggct aatttcaaga 698

cattttgatc tgaattggcc tcttttgaaa cactgattct agtttctata agagcaatcg 758

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<220>
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may be A, T, C, G, other or unknown
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Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
  1          5          10          15
tct gtt tct tct tct act act act tcc tct cct att cag tcg gag gct 155
Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala
          20          25          30

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Pro	Arg	Pro	Lys	Arg	Ala	Lys	Arg	Ala	Lys	Lys	Ser	Ser	Pro	Ser	Gly	
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gat	aaa	tct	cat	aac	ccg	aca	agc	cct	gct	tct	acc	cga	cgc	agc	tct	251
Asp	Lys	Ser	His	Asn	Pro	Thr	Ser	Pro	Ala	Ser	Thr	Arg	Arg	Ser	Ser	
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atc	tac	aga	gga	gtc	act	aga	cat	aga	tgg	act	ggg	aga	ttc	gag	gct	299
Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Phe	Glu	Ala	
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cat	ctt	tgg	gac	aaa	agc	tct	tgg	aat	tcg	att	cag	aac	aag	aaa	ggc	347
His	Leu	Trp	Asp	Lys	Ser	Ser	Trp	Asn	Ser	Ile	Gln	Asn	Lys	Lys	Gly	
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aaa	caa	gtt	tat	ctg	gga	gca	tat	gac	agt	gaa	gaa	gca	gca	gca	cat	395
Lys	Gln	Val	Tyr	Leu	Gly	Ala	Tyr	Asp	Ser	Glu	Glu	Ala	Ala	Ala	His	
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Thr	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Asp	Thr	Ile	Leu	
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aat	ttt	ccg	gca	gag	acg	tac	aca	aag	gaa	ttg	gaa	gaa	atg	cag	aga	491
Asn	Phe	Pro	Ala	Glu	Thr	Tyr	Thr	Lys	Glu	Leu	Glu	Glu	Met	Gln	Arg	
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Val	Thr	Lys	Glu	Glu	Tyr	Leu	Ala	Ser	Leu	Arg	Arg	Gln	Ser	Ser	Gly	
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Phe	Ser	Arg	Gly	Val	Ser	Lys	Tyr	Arg	Gly	Val	Ala	Arg	His	His	His	
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Asn	Gly	Arg	Trp	Glu	Ala	Arg	Ile	Gly	Arg	Val	Phe	Gly	Asn	Lys	Tyr	
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Leu	Tyr	Leu	Gly	Thr	Tyr	Asn	Thr	Gln	Glu	Glu	Ala	Ala	Ala	Ala	Tyr	
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gac	atg	gct	gcg	att	gag	tat	cga	ggc	gca	aac	gcg	gtt	act	aat	ttc	731
Asp	Met	Ala	Ala	Ile	Glu	Tyr	Arg	Gly	Ala	Asn	Ala	Val	Thr	Asn	Phe	
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gac	att	agt	aat	tac	att	gac	cgg	tta	aag	aag	aaa	ggt	gtt	ttc	ccg	779
Asp	Ile	Ser	Asn	Tyr	Ile	Asp	Arg	Leu	Lys	Lys	Lys	Gly	Val	Phe	Pro	
	225				230					235					240	
ttc	cct	gtg	aac	caa	gct	aac	cat	caa	gag	ggg	att	ctt	gtt	gaa	gcc	827
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<223> G979

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35 40 45

Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser  
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Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala  
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His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly  
85 90 95

Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His  
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Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu  
115 120 125

Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg  
130 135 140

Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly  
145 150 155 160

Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His  
165 170 175

Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr  
180 185 190

Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Tyr  
195 200 205

Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe  
210 215 220

Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro  
225 230 235 240

Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala  
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Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu  
260 265 270

Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Glu Lys  
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Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser  
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Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met  
305 310 315 320

Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys  
325 330 335

Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala  
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Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe  
355 360 365

Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu  
370 375 380

Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro  
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<222> (6)..(1088)

<223> G993

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Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys  
20 25 30

ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc 146  
Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser  
35 40 45

ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag 194  
Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu  
50 55 60

tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct 242  
Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro  
65 70 75



aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg	290
Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp	
80 85 90 95	
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Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile	
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gcc gtg agg aga ttc cgc gcc cgc gac gcc gtc act aac ttc aaa tct	386
Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser	
115 120 125	
caa gtt gat gga aac gac gcc gaa tcg gct ttt ctt gac gct cat tct	434
Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser	
130 135 140	
aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag	482
Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu	
145 150 155	
ttt gag cag agt aga cgg aag ttt gtt aac gcc gac gga aaa cgc tct	530
Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser	
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Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg	
180 185 190	
gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg	626
Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu	
195 200 205	
aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta	674
Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu	
210 215 220	
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Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly	
225 230 235	
gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt	770
Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg	
240 245 250 255	
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Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp	
260 265 270	
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Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys	
275 280 285	
ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa	914
Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys	
290 295 300	

00941519 09151600





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gct cca acg aac ccg act cat cat gag agt aat gct gcc aaa gag att 218  
 Ala Pro Thr Asn Pro Thr His His Glu Ser Asn Ala Ala Lys Glu Ile  
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cgt tac aga ggc gtt agg aaa cgt cca tgg gga aga tac gcc gct gag 266  
 Arg Tyr Arg Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala Ala Glu  
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atc cga gat ccg gtt aag aaa act cga gtc tgg ctc ggt acg ttc gac 314  
 Ile Arg Asp Pro Val Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp  
 50 55 60

acc gct cag cag gcg gcg cgt gct tac gac gca gcc gcg cgt gac ttt 362  
 Thr Ala Gln Gln Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Asp Phe  
 65 70 75

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 Arg Gly Val Lys Ala Lys Thr Asn Phe Gly Val Ile Val Gly Ser Ser  
 80 85 90

cct act cag agt agc acc gtc gtc gac tct ccc acg gcg gca ccg ttt 458  
 Pro Thr Gln Ser Ser Thr Val Val Asp Ser Pro Thr Ala Ala Arg Phe  
 95 100 105

ata aca cct ccg cac ctc gag ctc agc tta ggc ggc ggc ggc gcg tgt 506  
 Ile Thr Pro Pro His Leu Glu Leu Ser Leu Gly Gly Gly Gly Ala Cys  
 110 115 120 125

cgt cgt aag atc ccg ctt gtg cat ccg gtt tac tac tat aac atg gcg 554  
 Arg Arg Lys Ile Pro Leu Val His Pro Val Tyr Tyr Tyr Asn Met Ala  
 130 135 140

acg tat cca aag atg acg acg tgt ggt gtc cag agc gag tct gaa acg 602  
 Thr Tyr Pro Lys Met Thr Thr Cys Gly Val Gln Ser Glu Ser Glu Thr  
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tcg tcg gtc gtt gat ttc gaa ggt gga gct ggg aag ata tct ccg ccg 650  
 Ser Ser Val Val Asp Phe Glu Gly Gly Ala Gly Lys Ile Ser Pro Pro  
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 175 180 185

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&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

0034519-091300

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&lt;223&gt; G1020

&lt;400&gt; 38

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 35 40 45

Pro Val Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Gln  
 50 55 60

Gln Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Asp Phe Arg Gly Val  
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Lys Ala Lys Thr Asn Phe Gly Val Ile Val Gly Ser Ser Pro Thr Gln  
 85 90 95

Ser Ser Thr Val Val Asp Ser Pro Thr Ala Ala Arg Phe Ile Thr Pro  
 100 105 110

Pro His Leu Glu Leu Ser Leu Gly Gly Gly Gly Ala Cys Arg Arg Lys  
 115 120 125

Ile Pro Leu Val His Pro Val Tyr Tyr Tyr Asn Met Ala Thr Tyr Pro  
 130 135 140

Lys Met Thr Thr Cys Gly Val Gln Ser Glu Ser Glu Thr Ser Ser Val  
 145 150 155 160

Val Asp Phe Glu Gly Gly Ala Gly Lys Ile Ser Pro Pro Leu Asp Leu  
 165 170 175

Asp Leu Asn Leu Ala Pro Pro Ala Glu  
 180 185

&lt;210&gt; 39

&lt;211&gt; 1693

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (252)..(1247)

&lt;223&gt; G1023

&lt;220&gt;

<223> "n" at various positions throughout the sequence  
 may be A, T, C, G, other or unknown

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00994510-091366

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	Met	Ala	Glu	Arg	Lys	Lys	Arg	Ser	Ser	Ile	Gln	Thr	Asn			
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aaa	ccc	aac	aaa	aaa	ccc	atg	aag	aag	aaa	cct	ttt	cag	cta	aat	cac	338
Lys	Pro	Asn	Lys	Lys	Pro	Met	Lys	Lys	Lys	Pro	Phe	Gln	Leu	Asn	His	
	15					20					25					
ctc	cca	ggg	tta	tct	gaa	gat	ttg	aag	act	atg	aga	aaa	ctc	cgt	ttc	386
Leu	Pro	Gly	Leu	Ser	Glu	Asp	Leu	Lys	Thr	Met	Arg	Lys	Leu	Arg	Phe	
	30				35					40					45	
gtt	gtg	aat	gat	cct	tac	gct	act	gac	tac	tca	tca	agc	gaa	gaa	gaa	434
Val	Val	Asn	Asp	Pro	Tyr	Ala	Thr	Asp	Tyr	Ser	Ser	Ser	Glu	Glu	Glu	
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gaa	agg	agt	cag	aga	agg	aaa	cgt	tat	gtc	tgt	gag	atc	gat	ctt	cct	482
Glu	Arg	Ser	Gln	Arg	Arg	Lys	Arg	Tyr	Val	Cys	Glu	Ile	Asp	Leu	Pro	
			65					70					75			
ttc	gct	caa	gct	gct	act	caa	gca	gaa	tct	gaa	agc	tca	tat	tgt	cag	530
Phe	Ala		Gln	Ala	Ala	Thr	Gln	Ala	Glu	Ser	Glu	Ser	Ser	Tyr	Cys	Gln
		80						85					90			
gag	agt	aac	aat	aat	ggg	gta	agc	aag	act	aaa	atc	tca	gct	tgt	agc	578
Glu	Ser	Asn	Asn	Asn	Gly	Val	Ser	Lys	Thr	Lys	Ile	Ser	Ala	Cys	Ser	
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aaa	aag	gtt	tta	cgc	agc	aaa	gca	tct	ccg	gtc	gtt	gga	cgt	tct	tct	626
Lys	Lys	Val	Leu	Arg	Ser	Lys	Ala	Ser	Pro	Val	Val	Gly	Arg	Ser	Ser	
110					115					120					125	
act	act	gtc	tcg	aag	cct	gtt	ggg	gtt	agg	cag	agg	aaa	tgg	ggg	aaa	674
Thr	Thr	Val	Ser	Lys	Pro	Val	Gly	Val	Arg	Gln	Arg	Lys	Trp	Gly	Lys	
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tgg	gct	gct	gag	att	aga	cat	cca	atc	acc	aaa	gta	aga	act	tgg	ttg	722
Trp	Ala	Ala	Glu	Ile	Arg	His	Pro	Ile	Thr	Lys	Val	Arg	Thr	Trp	Leu	
			145					150					155			
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Gly	Thr	Tyr	Glu	Thr	Leu	Glu	Gln	Ala	Ala	Ala	Ala	Tyr	Ala	Thr	Lys	
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Lys	Leu	Glu	Phe	Asp	Ala	Leu	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Ser	Ser	
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Phe	Asp	Ala	Leu	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Ser	Ser	Val	Leu	Ser
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Ser Thr Ile Ala Asn Gln Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys  
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66160-61546660

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Ile 65	Lys	Arg	Gly	Arg	Phe 70	Ser	Pro	Asp	Glu	Glu 75	Gln	Thr	Ile	Leu	Asn 80
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Glu	His	Thr	Ile 165	Leu	Lys	Leu	Gln	Thr	Glu 170	Met	Ala	Lys	Leu	Gln 175	Leu
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 215 220 225

ttc ccg gag ttc gag tgg tcc gac tat ggt aat agt aat aat gat aat 897  
 Phe Pro Glu Phe Glu Trp Ser Asp Tyr Gly Asn Ser Asn Asn Asp Asn  
 230 235 240

aat aat ggt gtg gac aac att ata gag aac aat atg atg agc ctg tgg 945  
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Pro Glu Thr Asn Ile Ser Ser Gly Gln Gln Ala Met Gln Val Phe Thr
190 195 200

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Asp Val Ala Asp Lys Asn
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35 40 45
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Asp Gly Glu Asp Lys Asn Glu Thr Asp Ala Thr Val Ile Val Ala Asp
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 Gln Lys Tyr Phe Leu Arg Arg Thr Asn Leu Asn Arg Arg Arg Arg  
 145 150 155 160  
 Ser Ser Leu Phe Asp Ile Thr Thr Glu Thr Val Thr Glu Met Ala Met  
 165 170 175  
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 aag aaa gga cca tgg aca cca gag gaa gat atc atc ttg gtt tct tac 278  
 Lys Lys Gly Pro Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr  
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 Ile Gln Glu His Gly Pro Gly Asn Trp Arg Ser Val Pro Thr His Thr  
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 Gly Leu Arg Arg Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr  
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666160-15151660



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acc Thr 205	acc Thr	acc Thr	acc Thr	acc Thr	acc Thr 210	acg Thr	aga Arg	aac Asn	act Thr	aat Asn 215	cca Pro	tac Tyr	cca Pro	tct Ser	ggg Gly 220	854
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gac Asp	gga Gly 270	gaa Glu	ggg Gly	att Ile	gac Asp	cat His 275	tct Ser	ttg Leu	ttc Phe	agc Ser	ttc Phe 280	aac Asn	tcc Ser	ata Ile	gat Asp	1046

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 Val Leu Phe  
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Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly  
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Ile Lys Arg Gly Asn Phe Thr Glu His Glu Glu Lys Met Ile Leu His  
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Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu  
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Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu  
 100 105 110

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Lys Lys Lys Leu Lys Lys Met Asn Asp Ser Cys Asp Ser Thr Ile Asn  
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 Asn Gly Leu Asp Asn Lys Asp Phe Ser Ile Ser Asn Lys Asn Thr Thr  
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 Ser His Gln Ser Ser Asn Ser Ser Lys Gly Gln Trp Glu Arg Arg Leu  
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 Gln Thr Asp Ile Asn Met Ala Lys Gln Ala Leu Cys Asp Ala Leu Ser  
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 Ile Asp Lys Pro Gln Asn Pro Thr Asn Phe Ser Ile Pro Asp Leu Gly  
 180 185 190  
 Tyr Gly Pro Ser Ser Ser Ser Ser Ser Thr Thr Thr Thr Thr Thr Thr  
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 Thr Thr Thr Arg Asn Thr Asn Pro Tyr Pro Ser Gly Val Tyr Ala Ser  
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 may be A, T, C, G, other or unknown

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Trp	Thr	Asn	Tyr	Leu	Arg	Pro	Asp	Leu	Lys	Arg	Gly	Leu	Phe	Thr	Glu	
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Trp	Ser	Lys	Ile	Ala	Val	Glu	Leu	Pro	Gly	Arg	Thr	Asp	Asn	Asp	Ile	
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Lys	Asn	Tyr	Trp	Asn	Thr	His	Ile	Lys	Arg	Lys	Leu	Ile	Arg	Met	Gly	
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Glu	Glu	Thr	Ile	Leu	Val	Asn	Asp	Pro	Lys	Pro	Leu	Ser	Glu	Thr	Glu	
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gta	tct	gtt	gct	ttg	aag	aat	gac	acg	tca	gca	gtg	tta	tca	gga	aat	707
Val	Ser	Val	Ala	Leu	Lys	Asn	Asp	Thr	Ser	Ala	Val	Leu	Ser	Gly	Asn	
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Leu	Asn	Gln	Leu	Ala	Asp	Val	Asp	Gly	Asp	Asp	Gln	Pro	Trp	Ser	Phe	
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cta	atg	gaa	aat	gac	gaa	gga	gga	ggt	ggc	gac	gcc	gcc	gga	gag	ctt	803
Leu	Met	Glu	Asn	Asp	Glu	Gly	Gly	Gly	Gly	Asp	Ala	Ala	Gly	Glu	Leu	
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Gly Cys Phe Asp Val
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Glu Glu Ile Gln Leu Val Ile Asp Leu His Ala Arg Leu Gly Asn Arg
      85                90                95

Trp Ser Lys Ile Ala Val Glu Leu Pro Gly Arg Thr Asp Asn Asp Ile
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Lys Asn Tyr Trp Asn Thr His Ile Lys Arg Lys Leu Ile Arg Met Gly
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Ile Asp Pro Asn Thr His Arg Arg Phe Asp Gln Gln Lys Val Asn Glu
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Glu Glu Thr Ile Leu Val Asn Asp Pro Lys Pro Leu Ser Glu Thr Glu
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Leu Met Glu Asn Asp Glu Gly Gly Gly Asp Ala Ala Gly Glu Leu  
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Thr Met Leu Leu Ser Gly Asp Ile Thr Ser Ser Cys Ser Ser Ser Ser  
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Gly Leu Ile Glu Leu Glu Asn Ser Phe Ser Thr Gly Pro Met Met Thr	
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Glu His Gln Gln Ile Gln Glu Ser Asn Tyr Asn Asn Ser Thr Phe Phe	
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Pro Phe Thr Ile Ser Asn His Ser Asn Ser Ser Leu Tyr Ser Asp Ile	
290 295 300	
aaa tca gag acc aat ttt ttt ggc aca gag gct aca aat gtt ggt atg	1078
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Thr	Thr	Cys	Ser	Thr	Asn	Gln	Asn	Asn	Asn	Thr	Asp	His	Leu	Tyr	Thr
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Gly Leu Ile Glu Leu Glu Asn Ser Phe Ser Thr Gly Pro Met Met Thr  
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Glu His Gln Gln Ile Gln Glu Ser Asn Tyr Asn Asn Ser Thr Phe Phe  
260 265 270

Gly Asn Gly Asn Leu Asn Trp Gly Leu Thr Met Glu Glu Asn Gln Asn  
275 280 285

Pro Phe Thr Ile Ser Asn His Ser Asn Ser Ser Leu Tyr Ser Asp Ile  
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Lys Ser Glu Thr Asn Phe Phe Gly Thr Glu Ala Thr Asn Val Gly Met  
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Met Ala Ser Ser Ser Met Ser Thr Ser Ser Trp Thr Ala Arg  
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gag gac aag caa ttc gaa atg gcg ttg gcg aaa ttc gac aag gac act 159  
Glu Asp Lys Gln Phe Glu Met Ala Leu Ala Lys Phe Asp Lys Asp Thr  
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Pro Asp Arg Trp Gln Lys Ile Ala Arg Ala Val Gly Gly Lys Ser Thr  
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Glu Glu Val Lys Arg His Tyr Glu Leu Leu Leu Arg Asp Val Asn Asp  
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Lys Gly Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu Ile Asp Tyr Ile
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Asn Ile His Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Gly
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Ser	Ile	Tyr	Asn	Ser	Ser	His	His	His	His	His	His	His	Gln	Gln	His	
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Asn	His	Pro	Asn	Asn	Thr	His	Glu	Asn	Asn	Thr	Val	Asn	Gln	Thr	Glu	
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Gln	Ser	Trp	Phe	Pro	Ile	Met	Asp	Gln	Phe	Thr	Asn	Phe	Gln	Asp	Leu	
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Met	Pro	Met	Lys	Thr	Thr	Val	Gln	Asn	Ser	Leu	Ser	Tyr	Asp	Asp	Asp	
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Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro
  50          55          60
Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Thr Ile Ile
  65          70          75          80
Gln Leu His Ser Ile Met Gly Asn Lys Trp Ser Ala Ile Ala Ala Arg
  85          90          95
Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
  100          105          110
Ile Arg Lys Arg Leu Leu Lys Met Gly Ile Asp Pro Val Thr His Thr
  115          120          125
Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ser Ser Ser Ile
  130          135          140

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Tyr Asn Ser Ser His His His His His His His Gln Gln His Met Asn  
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 Trp Phe Pro Ile Met Asp Gln Phe Thr Asn Phe Gln Asp Leu Met Pro  
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 Lys Ser Asn Phe Val Leu Glu Pro Tyr Tyr Ser Asp Phe Ala Ser Val  
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 Leu Thr Thr Pro Ser Ser Ser Pro Thr Pro Leu Asn Ser Ser Ser Ser  
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 Met Gly Arg Gly Arg Ile  
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 gag att aag aag att gag aat atc aac agt cgt caa gtc act ttc tct 164  
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aag Lys	aga Arg	cga Arg 25	aac Asn	ggt Gly	ttg Leu	atc Ile	aag Lys 30	aag Lys	gct Ala	aaa Lys	gag Glu	ctt Leu 35	tcg Ser	att Ile	ctc Leu	212
tgt Cys	gac Asp 40	gcc Ala	gag Glu	gtt Val	gct Ala	ctt Leu 45	atc Ile	atc Ile	ttc Phe	tcc Ser 50	agc Ser	acc Thr	ggc Gly	aag Lys	att Ile	260
tac Tyr 55	gat Asp	ttc Phe	tcc Ser	agc Ser	gtc Val 60	tgt Cys	atg Met	gag Glu	caa Gln	att Ile 65	ctt Leu	tct Ser	aga Arg	tat Tyr	gga Gly 70	308
tac Tyr	act Thr	act Thr	gcg Ala	tcc Ser 75	act Thr	gag Glu	cat His	aaa Lys	caa Gln 80	caa Gln	aga Arg	gaa Glu	cac His	caa Gln 85	ctt Leu	356
cta Leu	att Ile	tgt Cys	gct Ala 90	tca Ser	cat His	gga Gly	aat Asn	gaa Glu 95	gct Ala	gtg Val	ttg Leu	cga Arg 100	aat Asn	gat Asp	gat Asp	404
tct Ser	atg Met	aag Lys 105	ggg Gly	gaa Glu	ctt Leu	gaa Glu 110	aga Arg	tta Leu	cag Gln	ctt Leu	gca Ala 115	att Ile	gag Glu	aga Arg	ctt Leu	452
aag Lys	ggt Gly 120	aag Lys	gag Glu	ctt Leu	gaa Glu	ggt Gly 125	atg Met	agt Ser	ttc Phe	ccg Pro	gat Asp 130	ctt Leu	att Ile	tct Ser	ctt Leu	500
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gca Ala	ttg Leu	gaa Glu	gaa Glu 170	aac Asn	caa Gln	atc Ile	ttg Leu 175	cgc Arg	aaa Lys	cag Gln	gtt Val	gag Glu 180	atg Met	ttg Leu	ggg Gly	644
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cca Pro	gaa Glu 200	gcc Ala	gat Asp	ccc Pro	gag Glu	agc Ser 205	tct Ser	tca Ser	tca Ser	gaa Glu 210	gag Glu	gat Asp	gag Glu	aat Asn	gac Asp	740
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Val	Leu	Arg	Asn	Asp	Asp	Ser	Met	Lys	Gly	Glu	Leu	Glu	Arg	Leu	Gln
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Gln Val Glu Met Leu Gly Arg Gly Ser Gly Pro Lys Val Leu Asn Glu  
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Glu Glu Asp Glu Asn Asp Asn Glu Glu His His Ser Asp Thr Ser Leu  
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 may be A, T, C, G, other or unknown

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 Met  
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gga agg ggc aag atc gcg att aag agg atc aat aac tct acg agc cgt 167  
 Gly Arg Gly Lys Ile Ala Ile Lys Arg Ile Asn Asn Ser Thr Ser Arg  
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cag gtt acg ttc tcg aag cga agg aat gga ttg ttg aag aaa gct aag 215  
 Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Lys  
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gag ctt gcg att ctc tgc gat gct gag gtt ggt gtc atc atc ttc tcc 263  
 Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe Ser  
 35 40 45

agc acc ggt agg ctc tac gat ttc tcc agc tcc agc atg aaa tcg gtc 311  
 Ser Thr Gly Arg Leu Tyr Asp Phe Ser Ser Ser Ser Met Lys Ser Val  
 50 55 60 65

ata gag aga tac agc gat gcc aaa gga gaa acc agt tca gaa aat gat 359  
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[illegible]



<223> G861

<223> "n" at various positions throughout the sequence  
may be A, T, C, G, other or unknown

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Glu Glu Leu Ser Val Leu Cys Asp Ala Asp Val Ala Leu Ile Ile Phe
          35             40             45

Ser Ser Thr Gly Lys Leu Phe Glu Phe Cys Ser Ser Ser Met Lys Glu
  50             55             60

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Val Leu Glu Arg His Asn Leu Gln Ser Lys Asn Leu Glu Lys Leu Asp  
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 85 90 95  
 Met Ser Lys Glu Ile Ala Asp Lys Ser His Arg Leu Arg Gln Met Arg  
 100 105 110  
 Gly Glu Glu Leu Gln Gly Leu Asp Ile Glu Glu Leu Gln Gln Leu Glu  
 115 120 125  
 Lys Ala Leu Glu Thr Gly Leu Thr Arg Val Ile Glu Thr Lys Ser Asp  
 130 135 140  
 Lys Ile Met Ser Glu Ile Ser Glu Leu Gln Lys Lys Gly Met Gln Leu  
 145 150 155 160  
 Met Asp Glu Asn Lys Arg Leu Arg Gln Gln Val Cys Val Leu Pro Ser  
 165 170 175  
 Leu Leu Ile Thr Asn Pro Phe Leu Leu Ser Thr Ile Asn Val His Thr  
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 Gln Glu Ala Ala Ser Gln Gly Leu Lys Ser Met Glu His Leu Ile Arg  
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aag Lys 130	agc Ser	tcg Ser	gag Glu	ggt Val 135	ggt Val	gag Glu	ttt Phe	gct Ala	aaa Lys	gag Glu 140	agc Ser	ttt Phe	agc Ser	gta Val 145	tct Ser	490
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tcc Ser 210	ggc Gly	aac Asn	ggc Gly	aag Lys	tgc Cys 215	cat His	tgc Cys	aag Lys	aaa Lys	agc Ser 220	cga Arg	aaa Lys	aat Asn	cgg Arg	atg Met 225	730
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cca Pro	cca Pro	gac Asp	gaa Glu 245	tat Tyr	tca Ser	tgg Trp	aga Arg	aag Lys 250	tat Tyr	gga Gly	caa Gln	aaa Lys 255	ccg Pro	atc Ile	aaa Lys	826
ggc Gly	tca Ser 260	cca Pro	cat His	cca Pro	cgg Arg	ggg Gly 265	tat Tyr	tac Tyr	aag Lys	tgt Cys	agt Ser 270	aca Thr	ttt Phe	aga Arg	gga Gly	874

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 Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ser Thr Met  
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Arg Lys Tyr Gly Gln Lys Leu Val Lys Gly Ser Glu Tyr Pro Arg Ser	
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Tyr Tyr Lys Cys Thr Asn Pro Asn Cys Gln Val Lys Lys Lys Val Glu	
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ttggaatctt ctgtgtaatc ttaagaagct ttaggaggta atgtaaaaaa ccagattcaa 1955

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00945-513660

Gly Asp Gly Gly Gly Ser Gly Gly Asp Val Asp Pro Arg Phe Lys Gln  
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 Ser Arg Pro Thr Gly Leu Met Ile Thr Gln Pro Pro Gly Met Phe Thr  
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 Val Pro Pro Gly Leu Ser Pro Ala Thr Leu Leu Asp Ser Pro Ser Phe  
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 Phe Gly Leu Phe Ser Pro Leu Gln Gly Thr Phe Gly Met Thr His Gln  
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 Gln Ala Leu Ala Gln Val Thr Ala Gln Ala Val Gln Gly Asn Asn Val  
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 His Met Gln Gln Ser Gln Gln Ser Glu Tyr Pro Ser Ser Thr Gln Gln  
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 Gln Gln Gln Gln Gln Gln Gln Ala Ser Leu Thr Glu Ile Pro Ser Phe  
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 Ser Ser Ala Pro Arg Ser Gln Ile Arg Ala Ser Val Gln Glu Thr Ser  
 210 215 220  
 Gln Gly Gln Arg Glu Thr Ser Glu Ile Ser Val Phe Glu His Arg Ser  
 225 230 235 240  
 Gln Pro Gln Asn Ala Asp Lys Pro Ala Asp Asp Gly Tyr Asn Trp Arg  
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 Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Asp Phe Pro Arg Ser Tyr  
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 Tyr Lys Cys Thr His Pro Ala Cys Pro Val Lys Lys Lys Val Glu Arg  
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 Ser Leu Asp Gly Gln Val Thr Glu Ile Ile Tyr Lys Gly Gln His Asn  
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 His Glu Leu Pro Gln Lys Arg Gly Asn Asn Asn Gly Ser Cys Lys Ser  
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 Ser Asp Ile Ala Asn Gln Phe Gln Thr Ser Asn Ser Ser Leu Asn Lys  
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 Ser Lys Arg Asp Gln Glu Thr Ser Gln Val Thr Thr Thr Glu Gln Met  
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His	Ser	Thr	Ser	Ser	Ala	Ala	Ser	Gln	Lys	Leu	Gln	Ser	Gln	Ile	Val	
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Lys	Asn	Thr	Gln	Pro	Glu	Ala	Pro	Ile	Val	Ser	Gln	Pro	Val	Arg	Thr	
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Thr	Thr	Asn	His	Pro	Gln	Ile	Val	Pro	Pro	Pro	Ser	Ser	Val	Thr	Leu	
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Asp	Phe	Ser	Lys	Pro	Ser	Ile	Phe	Gly	Thr	Lys	Ala	Lys	Ser	Ala	Glu	
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Leu	Glu	Phe	Ser	Lys	Glu	Asn	Phe	Ser	Val	Ser	Leu	Asn	Ser	Ser	Phe	
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Met	Ser	Ser	Ala	Ile	Thr	Gly	Asp	Gly	Ser	Val	Ser	Asn	Gly	Lys	Ile	
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Phe	Leu	Ala	Ser	Ala	Pro	Ser	Gln	Pro	Val	Asn	Ser	Ser	Gly	Lys	Pro	
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ccg	ttg	gct	ggc	cat	cct	tac	aga	aag	aga	tgt	ctc	gag	cat	gag	cac	684
Pro	Leu	Ala	Gly	His	Pro	Tyr	Arg	Lys	Arg	Cys	Leu	Glu	His	Glu	His	
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tca	gag	agt	ttc	tcc	gga	aaa	gtc	tcc	ggc	tcc	gcc	tac	gga	aag	tgc	732
Ser	Glu	Ser	Phe	Ser	Gly	Lys	Val	Ser	Gly	Ser	Ala	Tyr	Gly	Lys	Cys	
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cat	tgc	aag	aaa	agg	aaa	aat	cgg	atg	aag	aga	acc	gtg	aga	gta	ccg	780
His	Cys	Lys	Lys	Arg	Lys	Asn	Arg	Met	Lys	Arg	Thr	Val	Arg	Val	Pro	
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Ala	Ile	Ser	Ala	Lys	Ile	Ala	Asp	Ile	Pro	Pro	Asp	Glu	Tyr	Ser	Trp	
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Arg	Lys	Tyr	Gly	Gln	Lys	Pro	Ile	Lys	Gly	Ser	Pro	His	Pro	Arg	Gly	
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Tyr	Tyr	Lys	Cys	Ser	Thr	Phe	Arg	Gly	Cys	Pro	Ala	Arg	Lys	His	Val	
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gaa	cga	gca	tta	gat	gat	cca	gcg	atg	ctt	att	gtg	aca	tac	gaa	gga	972
Glu	Arg	Ala	Leu	Asp	Asp	Pro	Ala	Met	Leu	Ile	Val	Thr	Tyr	Glu	Gly	
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Ser Ala Ile Thr Gly Asp Gly Ser Val Ser Asn Gly Lys Ile Phe Leu  
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Ser	Asp	Val	Thr	Ile	Ile	Glu	His	Arg	Ser	Gln	Gln	Pro	Leu	Asn	Val
	210					215					220				
Asp	Lys	Pro	Ala	Asp	Asp	Gly	Tyr	Asn	Trp	Arg	Lys	Tyr	Gly	Gln	Lys
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Gln	Val	Lys	Gly	Ser	Glu	Phe	Pro	Arg	Ser	Tyr	Tyr	Lys	Cys	Thr	Asn
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Pro	Gly	Cys	Pro	Val	Lys	Lys	Lys	Val	Glu	Arg	Ser	Leu	Asp	Gly	Gln
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Val	Thr	Glu	Ile	Ile	Tyr	Lys	Gly	Gln	His	Asn	His	Glu	Pro	Pro	Gln
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Ser	Ile	Asn	Asn	Asn	Arg	Gly	Ser	Ser	Glu	Leu	Gly	Ala	Ser	Gln	Phe
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Gln	Thr	Asn	Ser	Ser	Asn	Lys	Thr	Lys	Arg	Glu	Gln	His	Glu	Ala	Val
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Ser	Gln	Ala	Thr	Thr	Thr	Glu	His	Leu	Ser	Glu	Ala	Ser	Asp	Gly	Glu
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Pro	Asp	Pro	Lys	Arg	Arg	Ser	Thr	Glu	Val	Arg	Ile	Ser	Glu	Pro	Ala
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Pro	Ala	Ala	Ser	His	Arg	Thr	Val	Thr	Glu	Pro	Arg	Ile	Ile	Val	Gln
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Thr	Thr	Ser	Glu	Val	Asp	Leu	Leu	Asp	Asp	Gly	Tyr	Arg	Trp	Arg	Lys
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Tyr	Gly	Gln	Lys	Val	Val	Lys	Gly	Asn	Pro	Tyr	Pro	Arg	Ser	Tyr	Tyr
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Lys	Cys	Thr	Thr	Pro	Gly	Cys	Gly	Val	Arg	Lys	His	Val	Glu	Arg	Ala
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Ala	Thr	Asp	Pro	Lys	Ala	Val	Val	Thr	Thr	Tyr	Glu	Gly	Lys	His	Asn
	450					455					460				
His	Asp	Leu	Pro	Ala	Ala	Lys	Ser	Ser	Ser	His	Ala	Ala	Ala	Ala	Ala
465					470					475					480







Asp Gln Glu Ile Ile Met Asp Ser Glu Lys Thr Leu Ala Ala Ser Thr  
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Ala Gln Asn His Val Asn Ala Met Val Gln Glu Gln Glu Asn Asn Thr  
245 250 255

Ser Ser Val Thr Ala Ile Asp Ala Gly Met Val Lys Glu Glu Gln Asn  
260 265 270

Asn Asn Gly Asp Gln Ser Lys Asp Tyr Tyr Glu Gly Ser Ser Thr Gly  
275 280 285

Glu Asp Leu Ser Leu Val Trp Gln Glu Thr Met Met Phe Asp Asp His  
290 295 300

Gln Asn His Tyr Tyr Cys Gly Glu Thr Ser Thr Thr Ser His Gln Phe  
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Gly Phe Ile Asp Asn Asp Asp Gln Phe Ser Ser Phe Phe Asp Ser Tyr  
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may be A, T, C, G, other or unknown

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cacacatata catccacaag aacccatatt gaagattcat cctacatata ttac atg 118  
Met  
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gat cag tac tca tcc tct ttg gtc gat act tca tta gat ctc act att 166  
Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr Ile  
5 10 15

ggc gtt act cgt atg cga gtt gaa gaa gat cca ccg aca agt gct ttg 214  
Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala Leu  
20 25 30

gtg gaa gaa tta aac cga gtt agt gct gag aac aag aag ctc tcg gag 262  
Val Glu Glu Leu Asn Arg Val Ser Ala Glu Asn Lys Lys Leu Ser Glu  
35 40 45

66160 61560

atg cta act ttg atg tgt gac aac tac aac gtc ttg agg aag caa ctt	310
Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln Leu	
50 55 60 65	
atg gaa tat gtt aac aag agc aac ata acc gag agg gat caa atc agc	358
Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile Ser	
70 75 80	
cct ccc aag aaa cgc aaa tcc ccg gcg aga gag gac gca ttc agc tgc	406
Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser Cys	
85 90 95	
gcg gtt att ggc gga gtg tcg gag agt agc tca acg gat caa gat gag	454
Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp Glu	
100 105 110	
tat ttg tgt aag aag cag aga gaa gag act gtc gtg aag gag aaa gtc	502
Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys Val	
115 120 125	
tca agg gtc tat tac aag acc gaa gct tct gac act acc ctc gtt gtg	550
Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val Val	
130 135 140 145	
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Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg Asp	
150 155 160	
aat cca tct cca aga gct tac ttc aaa tgt gct tgt gct cca agc tgt	646
Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser Cys	
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Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val Leu	
180 185 190	
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Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln Ile	
195 200 205	
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Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser Ala	
210 215 220 225	
tca aca ccc gtt gca gca aac aga aga agt agc ttg act gtg ccg gtg	838
Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro Val	
230 235 240	
act acc gta gat atg att gaa tcg aag aaa gtg acg agc cca acg tca	886
Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr Ser	
245 250 255	
aga atc gat ttt ccc caa gtt cag aaa ctt ttg gtg gag caa atg gct	934
Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met Ala	
260 265 270	

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Ser Ser Leu Thr Lys Asp Pro Asn Phe Thr Ala Ala Leu Ala Ala Ala
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gtt acc gga aaa ttg tat caa cag aat cat acc gag aaa tagtttagct 1031
Val Thr Gly Lys Leu Tyr Gln Gln Asn His Thr Glu Lys
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      35          40          45

Glu Met Leu Thr Leu Met Cys Asp Asn Tyr Asn Val Leu Arg Lys Gln
      50          55          60

Leu Met Glu Tyr Val Asn Lys Ser Asn Ile Thr Glu Arg Asp Gln Ile
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Ser Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser
      85          90          95

Cys Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp
      100          105          110

Glu Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys
      115          120          125

Val Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val
      130          135          140

Val Lys Asp Gly Tyr Gln Trp Arg Lys Tyr Gly Gln Lys Val Thr Arg
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Asp Asn Pro Ser Pro Arg Ala Tyr Phe Lys Cys Ala Cys Ala Pro Ser
      165          170          175

Cys Ser Val Lys Lys Lys Val Gln Arg Ser Val Glu Asp Gln Ser Val
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Leu Val Ala Thr Tyr Glu Gly Glu His Asn His Pro Met Pro Ser Gln  
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 Ile Asp Ser Asn Asn Gly Leu Asn Arg His Ile Ser His Gly Gly Ser  
 210 215 220  
 Ala Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro  
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 Val Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr  
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 Ser Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met  
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 Pro Phe Asp Leu His Phe Ser Gly Lys Leu Pro Lys Arg Glu Val Ser  
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gct tca gct tct aaa gtt gta gag aag aaa tgg tta gtg aaa gat gag 150  
 Ala Ser Ala Ser Lys Val Val Glu Lys Lys Trp Leu Val Lys Asp Glu  
 25 30 35 40

aag aga aat atg cta caa gat gaa ata aac cgg gtt aat tcg gag aac 198  
 Lys Arg Asn Met Leu Gln Asp Glu Ile Asn Arg Val Asn Ser Glu Asn  
 45 50 55

aag aag cta acc gaa atg tta gca aga gtc tgt gag aag tac tat gct 246  
 Lys Lys Leu Thr Glu Met Leu Ala Arg Val Cys Glu Lys Tyr Tyr Ala  
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Val	Asn	Phe	Gln	Asn	Lys	Gln	Leu	Thr	Gly	Lys	Arg	Lys	Gln	Glu	Leu	
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Asp	Glu	Phe	Val	Ser	Ser	Pro	Ile	Gly	Leu	Ser	Leu	Gly	Pro	Ile	Glu	
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Asn	Ile	Thr	Asn	Asp	Lys	Ala	Thr	Val	Ser	Thr	Ala	Tyr	Phe	Ala	Ala	
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Phe	Arg	Cys	Ser	Phe	Ser	Pro	Ser	Cys	Leu	Val	Lys	Lys	Lys	Val	Gln	
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Arg	Ser	Ala	Glu	Asp	Pro	Ser	Phe	Leu	Val	Ala	Thr	Tyr	Glu	Gly	Thr	
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His	Asn	His	Thr	Gly	Pro	His	Ala	Ser	Val	Ser	Arg	Thr	Val	Lys	Leu	
				205					210					215		
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Asp	Leu	Val	Gln	Gly	Gly	Leu	Glu	Pro	Val	Glu	Glu	Lys	Lys	Glu	Arg	
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Gly	Thr	Ile	Gln	Glu	Val	Leu	Val	Gln	Gln	Met	Ala	Ser	Ser	Leu	Thr	
		235					240					245				
aaa	gat	cct	aag	ttc	act	gca	gct	ctt	gcg	act	gct	att	tcc	ggg	aga	822
Lys	Asp	Pro	Lys	Phe	Thr	Ala	Ala	Leu	Ala	Thr	Ala	Ile	Ser	Gly	Arg	
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ttg	ata	gag	cat	tca	aga	aca	tgaaagttct	ctagaacatg	tatattttctg							873
Leu	Ile	Glu	His	Ser	Arg	Thr										
265					270											
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Ile	Asn 50	Arg	Val	Asn	Ser	Glu 55	Asn	Lys	Lys	Leu	Thr 60	Glu	Met	Leu	Ala
Arg 65	Val	Cys	Glu	Lys	Tyr 70	Tyr	Ala	Leu	Asn	Asn 75	Leu	Met	Glu	Glu	Leu 80
Gln	Ser	Arg	Lys	Ser 85	Pro	Glu	Ser	Val	Asn 90	Phe	Gln	Asn	Lys	Gln 95	Leu
Thr	Gly	Lys	Arg 100	Lys	Gln	Glu	Leu	Asp 105	Glu	Phe	Val	Ser	Ser 110	Pro	Ile
Gly	Leu 115	Ser	Leu	Gly	Pro	Ile	Glu 120	Asn	Ile	Thr	Asn 125	Asp	Lys	Ala	Thr
Val	Ser 130	Thr	Ala	Tyr	Phe	Ala 135	Ala	Glu	Lys	Ser	Asp 140	Thr	Ser	Leu	Thr
Val 145	Lys	Asp	Gly	Tyr	Gln 150	Trp	Arg	Lys	Tyr	Gly 155	Gln	Lys	Ile	Thr	Arg 160
Asp	Asn	Pro	Ser	Pro 165	Arg	Ala	Tyr	Phe	Arg 170	Cys	Ser	Phe	Ser	Pro 175	Ser
Cys	Leu	Val	Lys 180	Lys	Lys	Val	Gln	Arg	Ser 185	Ala	Glu	Asp	Pro 190	Ser	Phe
Leu	Val 195	Ala	Thr	Tyr	Glu	Gly	Thr 200	His	Asn	His	Thr	Gly 205	Pro	His	Ala
Ser	Val 210	Ser	Arg	Thr	Val	Lys 215	Leu	Asp	Leu	Val	Gln 220	Gly	Gly	Leu	Glu
Pro 225	Val	Glu	Glu	Lys	Lys 230	Glu	Arg	Gly	Thr	Ile 235	Gln	Glu	Val	Leu	Val 240
Gln	Gln	Met	Ala	Ser 245	Ser	Leu	Thr	Lys	Asp 250	Pro	Lys	Phe	Thr	Ala 255	Ala

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 Ser Ser Tyr Ser Gly Gly Gly Gly Gly Gly Asp Gly Phe Pro Ala Ile  
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gcc gcg gcg gcg aaa atg gaa gat acc gct ttg aga gaa gct gct tct 151  
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Gln Lys Asp Gly Leu Leu Leu Val Glu Ile Asp Arg Val Leu Lys Pro	
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gtg	aca	aac	aca	tgc	cta	aaa	caa	cag	tcg	aat	cct	cct	tct	cct	gct				104
Val	Thr	Asn	Thr	Cys	Leu	Lys	Gln	Gln	Ser	Asn	Pro	Pro	Ser	Pro	Ala				
5					10					15					20				
act	cct	gtg	gaa	agg	aag	gca	aga	ccg	gag	aaa	gac	cag	gct	ttg	aac				152
Thr	Pro	Val	Glu	Arg	Lys	Ala	Arg	Pro	Glu	Lys	Asp	Gln	Ala	Leu	Asn				
				25					30					35					
tgt	cca	aga	tgc	aac	tcc	tta	aac	acc	aag	ttc	tgt	tac	tac	aac	aac				200
Cys	Pro	Arg	Cys	Asn	Ser	Leu	Asn	Thr	Lys	Phe	Cys	Tyr	Tyr	Asn	Asn				
			40					45					50						
tac	agc	ctg	acg	cag	ccc	agg	tac	ttt	tgt	aaa	gac	tgc	agg	agg	tat				248
Tyr	Ser	Leu	Thr	Gln	Pro	Arg	Tyr	Phe	Cys	Lys	Asp	Cys	Arg	Arg	Tyr				
		55					60					65							
tgg	acc	gca	ggg	ggg	tcc	ctc	agg	aac	atc	ccc	gtc	ggg	ggc	ggc	gtc				296
Trp	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Asn	Ile	Pro	Val	Gly	Gly	Gly	Val				
	70					75				80									
cgc	aag	aac	aag	aga	tct	tct	tcc	aat	tcc	tct	tcc	tct	tca	ccc	tct				344
Arg	Lys	Asn	Lys	Arg	Ser	Ser	Ser	Asn	Ser	Ser	Ser	Ser	Ser	Pro	Ser				
85					90				95					100					
tcg	tct	tct	tct	tca	aag	aaa	cct	ctt	ttt	gcc	aac	aac	aac	acg	cct				392
Ser	Ser	Ser	Ser	Ser	Lys	Lys	Pro	Leu	Phe	Ala	Asn	Asn	Asn	Thr	Pro				
				105					110					115					
acg	cct	cct	ctt	cct	cat	ctt	aac	cct	aag	att	ggg	gaa	gca	gcc	gct				440
Thr	Pro	Pro	Leu	Pro	His	Leu	Asn	Pro	Lys	Ile	Gly	Glu	Ala	Ala	Ala				
			120					125				130							
act	aaa	gtt	caa	gac	ttg	acg	ttt	tct	caa	ggg	ttt	ggg	aac	gcc	cac				488
Thr	Lys	Val	Gln	Asp	Leu	Thr	Phe	Ser	Gln	Gly	Phe	Gly	Asn	Ala	His				
		135					140					145							
gag	gtt	aaa	gat	ctc	aac	ttg	gcg	ttt	tct	caa	ggg	ttt	ggg	atc	ggg				536
Glu	Val	Lys	Asp	Leu	Asn	Leu	Ala	Phe	Ser	Gln	Gly	Phe	Gly	Ile	Gly				
	150					155				160									
cac	aat	cat	cac	agt	agt	atc	cca	gag	ttt	ctg	caa	gta	gta	ccc	agc				584
His	Asn	His	His	Ser	Ser	Ile	Pro	Glu	Phe	Leu	Gln	Val	Val	Pro	Ser				
165					170				175						180				
agc	agt	atg	aag	a															



Gln Ala Leu Asn Cys Pro Arg Cys Asn Ser Leu Asn Thr Lys Phe Cys  
 35 40 45  
 Tyr Tyr Asn Asn Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Asp  
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 Cys Arg Arg Tyr Trp Thr Ala Gly Gly Ser Leu Arg Asn Ile Pro Val  
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 Gly Gly Gly Val Arg Lys Asn Lys Arg Ser Ser Ser Asn Ser Ser Ser  
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 Ser Ser Pro Ser Ser Ser Ser Ser Ser Ser Lys Lys Pro Leu Phe Ala Asn  
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 Phe Gly Ile Gly His Asn His His Ser Ser Ile Pro Glu Phe Leu Gln  
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 Val Val Pro Ser Ser Ser Met Lys Asn Asn Pro Leu Val Ser Thr Ser  
 180 185 190  
 Ser Ser Leu Glu Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Ser Asn  
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 Ser Arg Pro Ala Phe Met Ser Tyr Pro Asn Val His Asp Ser Ser Val  
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 Tyr Thr Ala Ser Gly Phe Gly Leu Ser Tyr Pro Gln Phe Gln Glu Phe  
 225 230 235 240  
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 245 250 255  
 Gln Glu Glu Gly Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro  
 260 265 270  
 Phe Glu Ser Leu Leu Lys Leu Pro Val Ser Ser Ser Ser Thr Asn Ser  
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 Gly Gly Asn Gly Asn Leu Lys Glu Asn Asn Asp Glu His Ser Asp His  
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 Glu His Glu Lys Glu Glu Gly Glu Ala Asp Gln Ser Val Gly Phe Trp  
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 caa gga ttc aat ttc atc aac caa act gtt tcg acg aga acg ata gat 630  
 Gln Gly Phe Asn Phe Ile Asn Gln Thr Val Ser Thr Arg Thr Ile Asp  
 185 190 195 200  
 gta ccg ttg gtg cct gaa agt gga gga gtg acg gcg gag atg acg aac 678  
 Val Pro Leu Val Pro Glu Ser Gly Gly Val Thr Ala Glu Met Thr Asn  
 205 210 215  
 acg gag acg cca gct gtg cag tta tca ccg gcg gag agg gaa gca agg 726  
 Thr Glu Thr Pro Ala Val Gln Leu Ser Pro Ala Glu Arg Glu Ala Arg  
 220 225 230  
 gtt ttg agg tat aga gag aag agg aag aat cgg aaa ttt gag aag acg 774  
 Val Leu Arg Tyr Arg Glu Lys Arg Lys Asn Arg Lys Phe Glu Lys Thr  
 235 240 245  
 att agg tat gcg tcg cgt aaa gct tac gct gag atg agg ccg aga atc 822  
 Ile Arg Tyr Ala Ser Arg Lys Ala Tyr Ala Glu Met Arg Pro Arg Ile  
 250 255 260  
 aaa gga cgt ttt gct aag aga aca gat tcg aga gag aat gat ggt gga 870  
 Lys Gly Arg Phe Ala Lys Arg Thr Asp Ser Arg Glu Asn Asp Gly Gly  
 265 270 275 280  
 gac gtc gga gtt tat ggc gga ttc ggt gtt gtt ccg agt ttc 912  
 Asp Val Gly Val Tyr Gly Gly Phe Gly Val Val Pro Ser Phe  
 285 290  
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 aattaaaact aaaatgtttc ctgatttaat caggggctaa gttattgtta gaagattggt 1032  
 gtttttttgaa ttaattctca caattgtatc cttaaattata tagtttactt aatgttgaac 1092  
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 35 40 45



Trp Leu Cys Glu Val Cys Glu Gln Ala Pro Ala His Val Thr Cys Lys  
 50 55 60  
 Ala Asp Ala Ala Ala Leu Cys Val Thr Cys Asp Arg Asp Ile His Ser  
 65 70 75 80  
 Ala Asn Pro Leu Ser Arg Arg His Glu Arg Val Pro Ile Thr Pro Phe  
 85 90 95  
 Tyr Asp Ala Val Gly Pro Ala Lys Ser Ala Ser Ser Ser Val Asn Phe  
 100 105 110  
 Val Asp Glu Asp Gly Gly Asp Val Thr Ala Ser Trp Leu Leu Ala Lys  
 115 120 125  
 Glu Gly Ile Glu Ile Thr Asn Leu Phe Ser Asp Leu Asp Tyr Pro Lys  
 130 135 140  
 Ile Glu Val Thr Ser Glu Glu Asn Ser Ser Gly Asn Asp Gly Val Val  
 145 150 155 160  
 Pro Val Gln Asn Lys Leu Phe Leu Asn Glu Asp Tyr Phe Asn Phe Asp  
 165 170 175  
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 180 185 190  
 Thr Val Ser Thr Arg Thr Ile Asp Val Pro Leu Val Pro Glu Ser Gly  
 195 200 205  
 Gly Val Thr Ala Glu Met Thr Asn Thr Glu Thr Pro Ala Val Gln Leu  
 210 215 220  
 Ser Pro Ala Glu Arg Glu Ala Arg Val Leu Arg Tyr Arg Glu Lys Arg  
 225 230 235 240  
 Lys Asn Arg Lys Phe Glu Lys Thr Ile Arg Tyr Ala Ser Arg Lys Ala  
 245 250 255  
 Tyr Ala Glu Met Arg Pro Arg Ile Lys Gly Arg Phe Ala Lys Arg Thr  
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 Gly Val Val Pro Ser Phe  
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666150:615150

&lt;223&gt; G902

&lt;400&gt; 109

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aagacttata agattgaaaa agcaag atg cgg att ttg tgc gat gct tgc gag 173
          Met Arg Ile Leu Cys Asp Ala Cys Glu
              1              5

aac gca gcc gca atc atc ttt tgc gcc gcc gat gaa gct gcc ctt tgt 221
Asn Ala Ala Ala Ile Ile Phe Cys Ala Ala Asp Glu Ala Ala Leu Cys
 10              15              20              25

cgc ccc tgc gat gaa aaa gtt cat atg tgc aac aag cta gct agt cgg 269
Arg Pro Cys Asp Glu Lys Val His Met Cys Asn Lys Leu Ala Ser Arg
              30              35              40

cat gta cgt gtt ggt tta gct gaa cca agc aat gcc cca tgc tgt gat 317
His Val Arg Val Gly Leu Ala Glu Pro Ser Asn Ala Pro Cys Cys Asp
              45              50              55

ata tgc gaa aat gca cct gcc ttc ttt tac tgt gag ata gac ggt agt 365
Ile Cys Glu Asn Ala Pro Ala Phe Phe Tyr Cys Glu Ile Asp Gly Ser
              60              65              70

tct ctt tgt ctg caa tgt gac atg gta gta cat gtt ggt ggc aag aga 413
Ser Leu Cys Leu Gln Cys Asp Met Val Val His Val Gly Gly Lys Arg
              75              80              85

aca cac ggt cgg ttt ctt ttg ctg aga cag aga atc gag ttt cca ggg 461
Thr His Gly Arg Phe Leu Leu Leu Arg Gln Arg Ile Glu Phe Pro Gly
 90              95              100              105

gat aag cct aaa gaa aac aat acg agg gac aat ttg cag aac caa aga 509
Asp Lys Pro Lys Glu Asn Asn Thr Arg Asp Asn Leu Gln Asn Gln Arg
              110              115              120

gtc tct aca aat gga aat ggt gaa gcc aat ggg aag att gat gac gaa 557
Val Ser Thr Asn Gly Asn Gly Glu Ala Asn Gly Lys Ile Asp Asp Glu
              125              130              135

atg att gat cta aat gct aat cca caa aga gta cat gag cca tca tca 605
Met Ile Asp Leu Asn Ala Asn Pro Gln Arg Val His Glu Pro Ser Ser
              140              145              150

aat aac aac ggg att gat gta aat aac gag aac aat cac gag cct gca 653
Asn Asn Asn Gly Ile Asp Val Asn Asn Glu Asn Asn His Glu Pro Ala
              155              160              165

ggc ctt gta cca gtt gga ccc ttt aaa cga gag tct gag aag 695
Gly Leu Val Pro Val Gly Pro Phe Lys Arg Glu Ser Glu Lys
 170              175              180

tgataagggtg agagagagag agagaaagag actctttact ctgattcaaa aaatcagttt 755

aagaagaaga ttgtaaaaag tttcaagaac tggagatttc atgtccgttt tttttccttc 815

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662160 " 61545660

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aaaaaaaaaa a

886

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<213> Arabidopsis thaliana

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<223> G902

<400> 110

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His Met Cys Asn Lys Leu Ala Ser Arg His Val Arg Val Gly Leu Ala  
35 40 45

Glu Pro Ser Asn Ala Pro Cys Cys Asp Ile Cys Glu Asn Ala Pro Ala  
50 55 60

Phe Phe Tyr Cys Glu Ile Asp Gly Ser Ser Leu Cys Leu Gln Cys Asp  
65 70 75 80

Met Val Val His Val Gly Gly Lys Arg Thr His Gly Arg Phe Leu Leu  
85 90 95

Leu Arg Gln Arg Ile Glu Phe Pro Gly Asp Lys Pro Lys Glu Asn Asn  
100 105 110

Thr Arg Asp Asn Leu Gln Asn Gln Arg Val Ser Thr Asn Gly Asn Gly  
115 120 125

Glu Ala Asn Gly Lys Ile Asp Asp Glu Met Ile Asp Leu Asn Ala Asn  
130 135 140

Pro Gln Arg Val His Glu Pro Ser Ser Asn Asn Asn Gly Ile Asp Val  
145 150 155 160

Asn Asn Glu Asn Asn His Glu Pro Ala Gly Leu Val Pro Val Gly Pro  
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Phe Lys Arg Glu Ser Glu Lys  
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<212> DNA

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&lt;222&gt; (130) .. (1272)

&lt;223&gt; G905

&lt;400&gt; 111

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tcctcatgaa accgggaagc ccaagtactt acttccacca tcaaatcgtc aaaccatttg 120
caaccatcg atg gtg gtc atg tca cga gta agc ttc tac tct tct ttc ttg 171
      Met Val Val Met Ser Arg Val Ser Phe Tyr Ser Ser Phe Leu
        1             5             10

cta cta ctg tta gag gtc gtt gtc gct agc agc gag ttt gat gat gaa 219
Leu Leu Leu Leu Glu Val Val Val Ala Ser Ser Glu Phe Asp Asp Glu
  15             20             25             30

gga aga aca tcg ttc agt cca acc acg gct ata atc atg atc gta ctc 267
Gly Arg Thr Ser Phe Ser Pro Thr Thr Ala Ile Ile Met Ile Val Leu
              35             40             45

gtt agt gtt ttc ttc gca ctt gga tgt atc tcc gtc tac atg agg agg 315
Val Ser Val Phe Phe Ala Leu Gly Cys Ile Ser Val Tyr Met Arg Arg
              50             55             60

tgt ctc cag cac gct ctg ggg atg gac agc ggt ggt ggt cca gga aac 363
Cys Leu Gln His Ala Leu Gly Met Asp Ser Gly Gly Gly Pro Gly Asn
        65             70             75

tgg ctt aac gtg agg caa acg acg gag cct ggg cta gac gcg tct gtt 411
Trp Leu Asn Val Arg Gln Thr Thr Glu Pro Gly Leu Asp Ala Ser Val
        80             85             90

ata gaa acg ttt cca acg ttt cct tac tct aca gtg aag acg ttg agg 459
Ile Glu Thr Phe Pro Thr Phe Pro Tyr Ser Thr Val Lys Thr Leu Arg
        95             100             105             110

atc ggt aaa gaa gct ttg gag tgt ccc gtt tgt ctc aac gag ttc gag 507
Ile Gly Lys Glu Ala Leu Glu Cys Pro Val Cys Leu Asn Glu Phe Glu
              115             120             125

gac gac gaa acg ctg cgt ttg att cct cag tgt tgt cac gtg ttt cat 555
Asp Asp Glu Thr Leu Arg Leu Ile Pro Gln Cys Cys His Val Phe His
              130             135             140

cct ggt tgc att gat gcc tgg ctc cgt tct cag acc aca tgt cct ctt 603
Pro Gly Cys Ile Asp Ala Trp Leu Arg Ser Gln Thr Thr Cys Pro Leu
              145             150             155

tgc cga gcc aat ctc gtt cct gta ccg ggt gag tct gtt tct tcg gag 651
Cys Arg Ala Asn Leu Val Pro Val Pro Gly Glu Ser Val Ser Ser Glu
        160             165             170

ata ccc ggt tta gct aga gaa acc ggt cag aac tct ctc aga acg ccg 699
Ile Pro Gly Leu Ala Arg Glu Thr Gly Gln Asn Ser Leu Arg Thr Pro
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Ile	Asp	Ser	Val	Ala	Trp	Thr	Gly	Asn	Gln	Ser	Met	Pro	Arg	Lys	Ser	
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atg	tct	aca	ggg	tgg	aaa	cta	gct	gaa	ttg	tac	agc	ccg	gct	agt	tca	843
Met	Ser	Thr	Gly	Trp	Lys	Leu	Ala	Glu	Leu	Tyr	Ser	Pro	Ala	Ser	Ser	
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ccg	ggc	caa	ccg	gag	gag	aat	ctc	gac	cgg	tat	acg	ctg	agg	tta	cca	891
Pro	Gly	Gln	Pro	Glu	Glu	Asn	Leu	Asp	Arg	Tyr	Thr	Leu	Arg	Leu	Pro	
			240				245				250					
caa	gag	ata	cat	gac	cag	ctt	gtg	aac	tcc	agc	ctg	gga	aag	caa	ggg	939
Gln	Glu	Ile	His	Asp	Gln	Leu	Val	Asn	Ser	Ser	Leu	Gly	Lys	Gln	Gly	
					260				265						270	
tca	aaa	ggc	caa	ctg	gcc	tta	cct	caa	gaa	agg	agc	tcg	gtt	aga	ggg	987
Ser	Lys	Gly	Gln	Leu	Ala	Leu	Pro	Gln	Glu	Arg	Ser	Ser	Val	Arg	Gly	
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Phe	Arg	Thr	Gly	Ser	Leu	Gly	Thr	Glu	Lys	Asn	Tyr	Phe	Tyr	Phe	Glu	
			290					295					300			
cgg	ttt	gat	caa	gac	ggg	cgg	ctg	gac	cgg	aga	cca	ttt	tct	ata	act	1083
Arg	Phe	Asp	Gln	Asp	Gly	Arg	Leu	Asp	Arg	Arg	Pro	Phe	Ser	Ile	Thr	
			305				310					315				
cct	cca	tac	cat	acc	cgg	tcg	ata	cag	tct	ccg	gat	gag	att	atc	aac	1131
Pro	Pro	Tyr	His	Thr	Arg	Ser	Ile	Gln	Ser	Pro	Asp	Glu	Ile	Ile	Asn	
			320				325				330					
gct	agt	ggg	aat	tat	cag	gat	cgt	gct	ggg	gca	cct	aaa	ggg	ttg	ctt	1179
Ala	Ser	Gly	Asn	Tyr	Gln	Asp	Arg	Ala	Gly	Ala	Pro	Lys	Gly	Leu	Leu	
					340				345						350	
cta	gca	ata	agg	tca	ccg	ttt	gat	cgg	tta	ttt	act	ggg	aag	aaa	aat	1227
Leu	Ala	Ile	Arg	Ser	Pro	Phe	Asp	Arg	Leu	Phe	Thr	Gly	Lys	Lys	Asn	
				355				360						365		
gcc	ggg	gag	cgt	tcg	tac	ctt	caa	tcc	ggc	gat	gcg	agc	cct	gtc		1272
Ala	Gly	Glu	Arg	Ser	Tyr	Leu	Gln	Ser	Gly	Asp	Ala	Ser	Pro	Val		
			370					375					380			
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&lt;211&gt; 381

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

<223> G905

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35 40 45

Val Phe Phe Ala Leu Gly Cys Ile Ser Val Tyr Met Arg Arg Cys Leu  
50 55 60

Gln His Ala Leu Gly Met Asp Ser Gly Gly Gly Pro Gly Asn Trp Leu  
65 70 75 80

Asn Val Arg Gln Thr Thr Glu Pro Gly Leu Asp Ala Ser Val Ile Glu  
85 90 95

Thr Phe Pro Thr Phe Pro Tyr Ser Thr Val Lys Thr Leu Arg Ile Gly  
100 105 110

Lys Glu Ala Leu Glu Cys Pro Val Cys Leu Asn Glu Phe Glu Asp Asp  
115 120 125

Glu Thr Leu Arg Leu Ile Pro Gln Cys Cys His Val Phe His Pro Gly  
130 135 140

Cys Ile Asp Ala Trp Leu Arg Ser Gln Thr Thr Cys Pro Leu Cys Arg  
145 150 155 160

Ala Asn Leu Val Pro Val Pro Gly Glu Ser Val Ser Ser Glu Ile Pro  
165 170 175

Gly Leu Ala Arg Glu Thr Gly Gln Asn Ser Leu Arg Thr Pro Ile Asp  
180 185 190

Asp Asn Arg Lys Arg Val Leu Thr Ser Pro Asp Glu Arg Leu Ile Asp  
195 200 205

Ser Val Ala Trp Thr Gly Asn Gln Ser Met Pro Arg Lys Ser Met Ser  
210 215 220

Thr Gly Trp Lys Leu Ala Glu Leu Tyr Ser Pro Ala Ser Ser Pro Gly  
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Gln Pro Glu Glu Asn Leu Asp Arg Tyr Thr Leu Arg Leu Pro Gln Glu  
245 250 255

Ile His Asp Gln Leu Val Asn Ser Ser Leu Gly Lys Gln Gly Ser Lys  
260 265 270

Gly Gln Leu Ala Leu Pro Gln Glu Arg Ser Ser Val Arg Gly Phe Arg  
275 280 285

Thr Gly Ser Leu Gly Thr Glu Lys Asn Tyr Phe Tyr Phe Glu Arg Phe  
 290 295 300  
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 Tyr His Thr Arg Ser Ile Gln Ser Pro Asp Glu Ile Ile Asn Ala Ser  
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 Gly Asn Tyr Gln Asp Arg Ala Gly Ala Pro Lys Gly Leu Leu Leu Ala  
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 Asp Phe Glu Asp Asp Ala Glu Gln Lys Phe His Tyr Lys Ser Glu Trp  
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 cac cgt tac aat ctc aag cgc aag ata gct ggt gtt cct gga gta aca 147  
 His Arg Tyr Asn Leu Lys Arg Lys Ile Ala Gly Val Pro Gly Val Thr  
 30 35 40  
 gag gca cta ttt gaa gct aga caa gct gct ata gct caa gag aag gtt 195  
 Glu Ala Leu Phe Glu Ala Arg Gln Ala Ala Ile Ala Gln Glu Lys Val  
 45 50 55  
 aaa gct gtt gaa gca ccg atg ctt tat agt tgt gga atc tgt aac aaa 243  
 Lys Ala Val Glu Ala Pro Met Leu Tyr Ser Cys Gly Ile Cys Asn Lys  
 60 65 70 75  
 ggt tac agg agt tcc aag gct cat gag cag cat ctt aag tcg aag agt 291  
 Gly Tyr Arg Ser Ser Lys Ala His Glu Gln His Leu Lys Ser Lys Ser  
 80 85 90  
 cat gtt ttg aag gct tcg acg agt act gga gag gag gat aaa gcg atc 339  
 His Val Leu Lys Ala Ser Thr Ser Thr Gly Glu Glu Asp Lys Ala Ile  
 95 100 105

66150: 5757660

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ttg aag ggt tcg att gag gag gaa gag agt gaa gat gaa tgg att gag	435
Leu Lys Gly Ser Ile Glu Glu Glu Glu Ser Glu Asp Glu Trp Ile Glu	
125 130 135	
gtt gat tcg gat gag gat ttg gat gcg gaa atg aat gag gat ggt gaa	483
Val Asp Ser Asp Glu Asp Leu Asp Ala Glu Met Asn Glu Asp Gly Glu	
140 145 150 155	
gaa gaa gat atg gat gaa gat ggt att gaa ttt gag ttg gat ccg gct	531
Glu Glu Asp Met Asp Glu Asp Gly Ile Glu Phe Glu Leu Asp Pro Ala	
160 165 170	
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Cys Cys Leu Met Cys Asp Lys Lys His Lys Thr Ile Glu Lys Cys Met	
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Val His Met His Lys Phe His Gly Phe Phe Ile Pro Asp Ile Glu Tyr	
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Leu Lys Asp Pro Lys Gly Phe Leu Thr Tyr Leu Gly Leu Lys Val Lys	
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Arg Asp Phe Val Cys Leu Tyr Cys Asn Glu Leu Cys His Pro Phe Ser	
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Ser Leu Glu Ala Val Arg Lys His Met Asp Ala Lys Gly His Cys Lys	
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Val His Tyr Gly Asp Gly Gly Asp Glu Glu Asp Ala Glu Leu Glu Glu	
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Phe Tyr Asp Tyr Ser Ser Ser Tyr Val Asn Gly Asp Glu Asn Gln Met	
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Glu Leu Val Ile Thr Lys Arg Thr Asp Asn Lys Val Thr Ser Arg Thr	
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Tyr	Leu	Lys	Arg	Cys	Val	Glu	Lys	Leu	Thr	Glu	Glu	Asn	Arg	Arg	Leu	
		195					200					205				
Gln	Lys	Glu	Ala	Met	Glu	Leu	Arg	Thr	Leu	Lys	Leu	Ser	Pro	Gln	Phe	
	210					215					220					
Tyr	Gly	Gln	Met	Thr	Pro	Pro	Thr	Thr	Leu	Ile	Met	Cys	Pro	Ser	Cys	
225					230					235					240	

Glu Arg Val Ala Gly Pro Ser Ser Ser Asn His His His Asn His Arg  
245 250 255

Pro Val Ser Ile Asn Pro Trp Ile Ala Cys Ala Gly Gln Val Ala His  
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1 5 10

cct tgg tgg aat gct ttt gga tct cag ccg ttg act aca gag agc ctt 159  
Pro Trp Trp Asn Ala Phe Gly Ser Gln Pro Leu Thr Thr Glu Ser Leu  
15 20 25

tcc ggc gaa gct tct gat tca ttc acc gga gtt aag gca gtt act acg 207  
Ser Gly Glu Ala Ser Asp Ser Phe Thr Gly Val Lys Ala Val Thr Thr  
30 35 40

gag gca gaa caa ggt gtg gtg gat aaa caa act tct aca act ctc ttc 255  
Glu Ala Glu Gln Gly Val Val Asp Lys Gln Thr Ser Thr Thr Leu Phe  
45 50 55 60

act ttc tca cct ggt ggt gaa aag agt tca aga gat gtg cca aag cct 303  
Thr Phe Ser Pro Gly Gly Glu Lys Ser Ser Arg Asp Val Pro Lys Pro  
65 70 75

cat gtt gct ttc gcg atg caa tca gct tgc ttc gag ttt gga ttt gct 351  
His Val Ala Phe Ala Met Gln Ser Ala Cys Phe Glu Phe Gly Phe Ala  
80 85 90

cag cca atg atg tac aca aag cat cct cat gtt gaa caa tac tat gga 399  
Gln Pro Met Met Tyr Thr Lys His Pro His Val Glu Gln Tyr Tyr Gly  
95 100 105

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Val Val Ser Ala Tyr Gly Ser Gln Arg Ser Ser Gly Arg Val Met Ile  
110 115 120

cca ctg aag atg gag aca gaa gaa gat ggt acc atc tat gtg aac tca 495  
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00304549-09199

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Leu His Ala Met Arg Arg Pro Arg Gly Ser Gly Gly Arg Phe Leu Asn  
175 180 185  
  
acc aag aca gct gat gcg gct aag cag tct aag ccg agt aat tct cag 687  
Thr Lys Thr Ala Asp Ala Ala Lys Gln Ser Lys Pro Ser Asn Ser Gln  
190 195 200  
  
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Ser Ser Glu Val Phe His Pro Glu Asn Glu Thr Ile Asn Ser Ser Arg  
205 210 215 220  
  
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225 230 235  
  
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Tyr Phe Leu Ser Ser Ser Ala Tyr Ser Pro Gly Gly Met Val Met Pro  
240 245 250  
  
atc aag tgg aat gca gca gca atg gat att ggc tgc tgc aaa ctt aat 879  
Ile Lys Trp Asn Ala Ala Ala Met Asp Ile Gly Cys Cys Lys Leu Asn  
255 260 265  
  
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<223> G1334

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 Ser Asp Ser Phe Thr Gly Val Lys Ala Val Thr Thr Glu Ala Glu Gln  
 35 40 45  
 Gly Val Val Asp Lys Gln Thr Ser Thr Thr Leu Phe Thr Phe Ser Pro  
 50 55 60  
 Gly Gly Glu Lys Ser Ser Arg Asp Val Pro Lys Pro His Val Ala Phe  
 65 70 75 80  
 Ala Met Gln Ser Ala Cys Phe Glu Phe Gly Phe Ala Gln Pro Met Met  
 85 90 95  
 Tyr Thr Lys His Pro His Val Glu Gln Tyr Tyr Gly Val Val Ser Ala  
 100 105 110  
 Tyr Gly Ser Gln Arg Ser Ser Gly Arg Val Met Ile Pro Leu Lys Met  
 115 120 125  
 Glu Thr Glu Glu Asp Gly Thr Ile Tyr Val Asn Ser Lys Gln Tyr His  
 130 135 140  
 Gly Ile Ile Arg Arg Arg Gln Ser Arg Ala Lys Ala Glu Lys Leu Ser  
 145 150 155 160  
 Arg Cys Arg Lys Pro Tyr Met His His Ser Arg His Leu His Ala Met  
 165 170 175  
 Arg Arg Pro Arg Gly Ser Gly Gly Arg Phe Leu Asn Thr Lys Thr Ala  
 180 185 190  
 Asp Ala Ala Lys Gln Ser Lys Pro Ser Asn Ser Gln Ser Ser Glu Val  
 195 200 205  
 Phe His Pro Glu Asn Glu Thr Ile Asn Ser Ser Arg Glu Ala Asn Glu  
 210 215 220  
 Ser Asn Leu Ser Asp Ser Ala Val Thr Ser Met Asp Tyr Phe Leu Ser  
 225 230 235 240  
 Ser Ser Ala Tyr Ser Pro Gly Gly Met Val Met Pro Ile Lys Trp Asn  
 245 250 255  
 Ala Ala Ala Met Asp Ile Gly Cys Cys Lys Leu Asn Ile  
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&lt;211&gt; 1530

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

0904519-094560





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 210 215 220

gag aag aaa cgt agc tgt cgc cga cct ctc tca gat cac aat gca aga 780  
 Glu Lys Lys Arg Ser Cys Arg Arg Pro Leu Ser Asp His Asn Ala Arg  
 225 230 235

cgt cgc aag cca aat cct gga agg aca tat gat ggg aaa cca cag gtg 828  
 Arg Arg Lys Pro Asn Pro Gly Arg Thr Tyr Asp Gly Lys Pro Gln Val  
 240 245 250 255

gat ttt gta tgg aac aga ttt gca ctt atc cat cca aga agt gag gaa 876  
 Asp Phe Val Trp Asn Arg Phe Ala Leu Ile His Pro Arg Ser Glu Glu  
 260 265 270

aag ttt cta tgg ccc agt tca aag cct gta cca tca aga gtc tta atg 924  
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 275 280 285

ccg cag cct gca aag acc gag att tcc aat aag ctg ttc acc gag cac 972  
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 Ser Arg Phe Gly Leu Leu Asp Pro Lys Thr Lys Ser Ala Arg Ala Glu  
 305 310 315

tta ttc agt aaa gaa aag gtc aca atc tct tca cac atg ggt gct tct 1068  
 Leu Phe Ser Lys Glu Lys Val Thr Ile Ser Ser His Met Gly Ala Ser  
 320 325 330 335

caa gat ctt gat ggt gct ctc tct ctt ctg tca aat tca aca aca tgg 1116  
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 340 345 350

gtt tct tcc tct gac caa cca aga cgt ttt acc ctt gat cac cat ccc 1164  
 Val Ser Ser Ser Asp Gln Pro Arg Arg Phe Thr Leu Asp His His Pro  
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 Ser Ser Asn Leu Gln Pro Val Ala Asn Arg Ser Ala Ala Gln Leu Ser  
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 385 390 395

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 Thr Ala Leu His Arg Asn Gly Ala Gly Gln Phe Asn Glu Asn Tyr Phe  
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agc ttg aac cag ttt tat aac tgaaagctgt atgccttta atcctattta 1359  
 Ser Leu Asn Gln Phe Tyr Asn  
 420

ggatcaagca agctagtgat aagttaagat aggagctgtg aaacttgcaa gacaccaa 1419





gaa Glu	ctt Leu	gtg Val	gtt Val	caa Gln 30	tac Tyr	ctt Leu	aag Lys	agg Arg	aaa Lys 35	gtt Val	tgt Cys	tct Ser	tct Ser	cct Pro 40	ttg Leu	147
cca Pro	gct Ala	tca Ser	atc Ile 45	atc Ile	cct Pro	gag Glu	ttt Phe	gat Asp 50	gtt Val	tgc Cys	aga Arg	gct Ala	gat Asp 55	cct Pro	tgg Trp	195
gat Asp	tta Leu	cct Pro 60	cgc Arg	aat Asn	ttg Leu	gag Glu	aaa Lys 65	gag Glu	agg Arg	tac Tyr	ttc Phe	ttt Phe 70	agc Ser	aca Thr	agg Arg	243
gaa Glu	gct Ala 75	aaa Lys	tac Tyr	cca Pro	aat Asn	ggg Gly 80	aac Asn	cgg Arg	tct Ser	aac Asn	cgg Arg 85	gca Ala	act Thr	ggg Gly	tct Ser	291
ggc Gly 90	tat Tyr	tgg Trp	aaa Lys	gct Ala	acc Thr 95	ggc Gly	att Ile	gat Asp	aaa Lys	cgg Arg 100	ggt Val	gtg Val	acc Thr	tct Ser	aga Arg 105	339
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aaa Lys	cca Pro	cct Pro	cat His 125	ggc Gly	tca Ser	aga Arg	acc Thr	gat Asp 130	tgg Trp	atc Ile	atg Met	cac His	gaa Glu 135	tat Tyr	cgc Arg	435
ctc Leu	tct Ser	tct Ser 140	tct Ser	cct Pro	ccg Pro	agt Ser	tct Ser 145	atg Met	ggc Gly	ccc Pro	act Thr	cag Gln 150	aac Asn	tgg Trp	gta Val	483
ctc Leu	tgt Cys 155	cgt Arg	atc Ile	ttc Phe	ttg Leu	aag Lys 160	aaa Lys	aga Arg	gcc Ala	ggc Gly	aac Asn 165	aag Lys	aac Asn	gac Asp	gac Asp	531
gac Asp 170	gac Asp	gga Gly	gat Asp	agc Ser	cgt Arg 175	aat Asn	ctt Leu	aga Arg	cat His	aat Asn 180	aat Asn	aat Asn	aac Asn	aat Asn	tcg Ser 185	579
agt Ser	gac Asp	caa Gln	att Ile	gag Glu 190	ata Ile	att Ile	aca Thr	aca Thr	gac Asp 195	caa Gln	aca Thr	gat Asp	gat Asp	aaa Lys 200	aca Thr	627
aaa Lys	cca Pro	atc Ile	ttc Phe 205	ttt Phe	gat Asp	ttc Phe	atg Met	aga Arg 210	aaa Lys	gaa Glu	aga Arg	aca Thr	aca Thr 215	gat Asp	ttg Leu	675
aac Asn	ctt Leu	ttg Leu 220	ccg Pro	agc Ser	tct Ser	cct Pro	tct Ser 225	tcc Ser	gat Asp	cat His	gct Ala	tca Ser 230	agt Ser	gga Gly	gtc Val	723
acg Thr	acg Thr 235	gag Glu	atc Ile	ttc Phe	tct Ser	tct Ser	tcc Ser 240	gat Asp	gaa Glu	gag Glu	acc Thr 245	agt Ser	agt Ser	tgc Cys	aat Asn	771



Met Arg Lys Glu Arg Thr Thr Asp Leu Asn Leu Leu Pro Ser Ser Pro  
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<223> G462

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Thr Glu Leu Arg Leu Gly Leu Pro Gly Arg Asp Val Ala Glu Lys Met 25  
15 20

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Met Lys Lys Arg Ala Phe Thr Glu Met Asn Met Thr Ser Ser Gly Ser 40  
30 35

aat agt gat caa tgt gaa agc ggc gtc gtt tca tct ggt ggt gac gct 195  
Asn Ser Asp Gln Cys Glu Ser Gly Val Val Ser Ser Gly Gly Asp Ala 55  
45 50

gag aag gtt aat gat tcg ccg gcg gcg aaa agc cag gtg gtg ggg tgg 243  
Glu Lys Val Asn Asp Ser Pro Ala Ala Lys Ser Gln Val Val Gly Trp 70  
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cca ccg gtt tgt tct tac cgg aag aaa aac agc tgt aag gaa gct tcg 291  
Pro Pro Val Cys Ser Tyr Arg Lys Lys Asn Ser Cys Lys Glu Ala Ser 90  
75 80 85

acc acg aaa gtg ggg tta ggg tat gtg aaa gtg agc atg gat ggt gtg 339  
Thr Thr Lys Val Gly Leu Gly Tyr Val Lys Val Ser Met Asp Gly Val 105  
95 100

cct tat ttg agg aag atg gat ctt ggt tcg agc caa ggc tat gat gat 387  
Pro Tyr Leu Arg Lys Met Asp Leu Gly Ser Ser Gln Gly Tyr Asp Asp 120  
110 115

cta gcc ttt gct ctt gat aag ctc ttc ggt ttc cgt ggc atc ggt gtg 435  
Leu Ala Phe Ala Leu Asp Lys Leu Phe Gly Phe Arg Gly Ile Gly Val 135  
125 130

0004410-6754660

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140 145 150

aaa gat gga gac tgg atg ctc gcc ggt gat gta cct tgg ggg atg ttt 531  
Lys Asp Gly Asp Trp Met Leu Ala Gly Asp Val Pro Trp Gly Met Phe  
155 160 165 170

cta gag tca tgc aag agg ttg aga ata atg aaa aga tcg gat gct acc 579  
Leu Glu Ser Cys Lys Arg Leu Arg Ile Met Lys Arg Ser Asp Ala Thr  
175 180 185

ggg ttt ggg ctg cag cct aga gga gta gac gag tgatgatgac ttgaacaaga 632  
Gly Phe Gly Leu Gln Pro Arg Gly Val Asp Glu  
190 195

agcaaggagc tgggttcatta atttaatctt aaacttgatc atcaagatcc tttagaacat 692

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catgttaaaaa aaaaaaaaaa aaaaaaa 779

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<213> Arabidopsis thaliana

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<223> G462

<400> 136

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35 40 45

Ser Gly Val Val Ser Ser Gly Gly Asp Ala Glu Lys Val Asn Asp Ser  
50 55 60

Pro Ala Ala Lys Ser Gln Val Val Gly Trp Pro Pro Val Cys Ser Tyr  
65 70 75 80

Arg Lys Lys Asn Ser Cys Lys Glu Ala Ser Thr Thr Lys Val Gly Leu  
85 90 95

Gly Tyr Val Lys Val Ser Met Asp Gly Val Pro Tyr Leu Arg Lys Met  
100 105 110

Asp Leu Gly Ser Ser Gln Gly Tyr Asp Asp Leu Ala Phe Ala Leu Asp  
115 120 125

Lys Leu Phe Gly Phe Arg Gly Ile Gly Val Ala Leu Lys Asp Gly Asp  
130 135 140

Asn Cys Glu Tyr Val Thr Ile Tyr Glu Asp Lys Asp Gly Asp Trp Met  
145 150 155 160

Leu Ala Gly Asp Val Pro Trp Gly Met Phe Leu Glu Ser Cys Lys Arg  
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Arg Gly Val Asp Glu  
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tcaatttgat cgtcctgaat tcatcgtcct atttaggggt tcgatcacia tctgaagagg 180

aggtc atg gac gtt tct gct aga aag tca caa aaa gct ggg cgc gaa aag 230

Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys  
1 5 10 15

ttg agg agg gaa aaa ctg aat gag cat ttt gtt gaa ctg gga aat gta 278

Leu Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val  
20 25 30

ctc gat cca gag aga ccc aag aat gac aaa gcc acg att ctg act gat 326

Leu Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp  
35 40 45

act gtt cag ttg ttg aaa gag ctc aca tct gaa gtc aac aaa ctg aaa 374

Thr Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys  
50 55 60

tct gag tac acc gca ttg aca gat gag tcc cgc gag ttg aca cag gag 422

Ser Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu  
65 70 75

aaa aac gac ctg aga gaa gaa aag aca tcg ctg aaa tca gat ata gag 470

Lys Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu  
80 85 90 95

aat ctc aat ctt caa tac cag cag aga tta agg tca atg tct cca tgg 518

Asn Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp  
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&lt;223&gt; G782

&lt;400&gt; 138

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Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp Thr
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Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser
 50              55              60

Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys
 65              70              75              80

Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn
          85              90              95

Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly
          100              105              110

Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe Pro
 115              120              125

Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro
 130              135              140

Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile
 145              150              155              160

Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val
          165              170              175

Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser
 180              185              190

Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala
 195              200              205

Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly
 210              215              220

Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg
 225              230              235              240

Cys Lys Arg Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His Ser
          245              250              255

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Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys
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090410 16154660

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1 5 10																
gaa gca aat gct act gca gat gaa aga tgt aga aaa ggt aaa gta ccg 161																
Glu Ala Asn Ala Thr Ala Asp Glu Arg Cys Arg Lys Gly Lys Val Pro																
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45 50 55																
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gac gtg ttt ggt caa att gag tct ctt aga aag gag cat gct tct ctc 353																
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80 85 90																
cta tct gaa tct agc tat gta acc aca gag aag aat gag ctc aag gaa 401																
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95 100 105																
gaa aca tca gtg ctt gag act gag att tcg aaa cta caa aac gag att 449																
Glu Thr Ser Val Leu Glu Thr Glu Ile Ser Lys Leu Gln Asn Glu Ile																
110 115 120																
gaa gct aga gcg aat cag tcg aaa cct gac ttg aac acc tct cct gca 497																
Glu Ala Arg Ala Asn Gln Ser Lys Pro Asp Leu Asn Thr Ser Pro Ala																
125 130 135																
ccc gag tac cat cat cat cat tat caa caa caa cat cct gaa cgt gta 545																
Pro Glu Tyr His His His His Tyr Gln Gln Gln His Pro Glu Arg Val																
140 145 150 155																
tct cag ttc cca gga ctt ccc att ttc caa ggc ccc ggc ttt caa caa 593																
Ser Gln Phe Pro Gly Leu Pro Ile Phe Gln Gly Pro Gly Phe Gln Gln																
160 165 170																

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 Ser Ala Thr Thr Leu His Pro Pro Ala Thr Val Leu Val Leu Pro Ile  
                   175                                  180                                  185

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                   190                                  195                                  200

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 Gln Pro Leu Met Phe Asn Ser Ser Asn Val Ser Asn Pro Cys Pro Arg  
                   205                                  210                                  215

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 Tyr Ala Ser Ala Ala Asp Ser Trp Ser Ser Arg Leu Leu Gly Glu Arg  
                   220                                  225                                  230                                  235

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 Leu Lys Ala Ser Glu  
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Ala Val Arg Glu Arg Leu Lys Arg Glu His Leu Asn Glu Leu Phe Ile  
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Glu Leu Ala Asp Thr Leu Glu Leu Asn Gln Gln Asn Ser Gly Lys Ala  
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Ser Ile Leu Cys Glu Ala Thr Arg Phe Leu Lys Asp Val Phe Gly Gln  
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Ile Glu Ser Leu Arg Lys Glu His Ala Ser Leu Leu Ser Glu Ser Ser  
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Gly Asp Arg Asn Met His Asn Pro Tyr Ala Ser Gly Ser Ser Tyr Asp	
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Ala Leu Phe Pro Pro Cys Ala Lys Leu Pro Tyr His Gly Val Glu Leu	
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caa ccg tct gcg gtc tgt cca aag aac ttt gtc atc ttc gat caa aca	615
Gln Pro Ser Ala Val Cys Pro Lys Asn Phe Val Ile Phe Asp Gln Thr	
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tat gac cgc agc caa gtg atg tac cat cct gag ctg act cat aag ctc	663
Tyr Asp Arg Ser Gln Val Met Tyr His Pro Glu Leu Thr His Lys Leu	
65 70 75	
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Met Asn Thr Pro Ser Leu Asn Asn Leu Ala Ser Thr Phe Gln Asn Glu	
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tat gtt ggg gga agt tat ggt aac tat ggt aac tat gag caa gaa gta	759
Tyr Val Gly Gly Ser Tyr Gly Asn Tyr Gly Asn Tyr Glu Gln Glu Val	
95 100 105	
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Ser Ser Ser Tyr Gln Glu Asp Pro Asn Glu Ile Asp Ala Leu Leu Ser	
110 115 120 125	
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Ala Asp Glu Asp Tyr Glu Glu Asn Asp Asp Asn Glu Gly Glu Glu Asp	
130 135 140	
ggt ggt gat tca gaa gaa gtc agc act gct cgt act tct tcc agg gat	903
Gly Gly Asp Ser Glu Glu Val Ser Thr Ala Arg Thr Ser Ser Arg Asp	
145 150 155	
tat gga aac acc aca gca gaa tct tgt tgt tcc agt tat ggt tac aac	951
Tyr Gly Asn Thr Thr Ala Glu Ser Cys Cys Ser Ser Tyr Gly Tyr Asn	
160 165 170	
aac aac aac aac aac aac tca agg aag cag agt tta tcg ggc agt gct	999
Asn Asn Asn Asn Asn Asn Ser Arg Lys Gln Ser Leu Ser Gly Ser Ala	
175 180 185	
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Ser Ser Ser Asn Asn Asp Gly Lys Gly Arg Lys Lys Met Lys Lys Met	
190 195 200 205	
atg gga gta ttg agg aga att gtc cct gga gga gaa cag atg aat aca	1095
Met Gly Val Leu Arg Arg Ile Val Pro Gly Gly Glu Gln Met Asn Thr	
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gct tgc gtt ctt gat gaa gct gtt cag tat ctc aag tca ctt aaa atc	1143
Ala Cys Val Leu Asp Glu Ala Val Gln Tyr Leu Lys Ser Leu Lys Ile	
225 230 235	

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 Pro Pro Cys Ala Lys Leu Pro Tyr His Gly Val Glu Leu Gln Pro Ser  
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 Ser Gln Val Met Tyr His Pro Glu Leu Thr His Lys Leu Met Asn Thr  
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 Pro Ser Leu Asn Asn Leu Ala Ser Thr Phe Gln Asn Glu Tyr Val Gly  
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 Tyr Gln Glu Asp Pro Asn Glu Ile Asp Ala Leu Leu Ser Ala Asp Glu  
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 Asp Tyr Glu Glu Asn Asp Asp Asn Glu Gly Glu Glu Asp Gly Gly Asp  
                                   130                                  135                                  140  
 Ser Glu Glu Val Ser Thr Ala Arg Thr Ser Ser Arg Asp Tyr Gly Asn  
       145                                  150                                  155                                  160  
 Thr Thr Ala Glu Ser Cys Cys Ser Ser Tyr Gly Tyr Asn Asn Asn Asn  
                                   165                                  170                                  175

Asn Asn Asn Ser Arg Lys Gln Ser Leu Ser Gly Ser Ala Ser Ser Ser  
180 185 190

Asn Asn Asp Gly Lys Gly Arg Lys Lys Met Lys Lys Met Met Gly Val  
195 200 205

Leu Arg Arg Ile Val Pro Gly Gly Glu Gln Met Asn Thr Ala Cys Val  
210 215 220

Leu Asp Glu Ala Val Gln Tyr Leu Lys Ser Leu Lys Ile Glu Ala Gln  
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ctttactcgt ttccttc atg gct aat aac aac aac atc cca cat gat agc 170  
Met Ala Asn Asn Asn Asn Ile Pro His Asp Ser  
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atc tcc gat cca tct cct acc gac gat ttc ttc gag cag atc ctc ggg 218  
Ile Ser Asp Pro Ser Pro Thr Asp Asp Phe Phe Glu Gln Ile Leu Gly  
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ctt tcc aac ttc tcc ggt tct tca ggt tct ggt ctc tct gga atc ggc 266  
Leu Ser Asn Phe Ser Gly Ser Ser Gly Ser Gly Leu Ser Gly Ile Gly  
30 35 40

ggc gtg ggt cca cct ccg atg atg ctt cag ctt ggt tca ggc aac gaa 314  
Gly Val Gly Pro Pro Pro Met Met Leu Gln Leu Gly Ser Gly Asn Glu  
45 50 55

ggg aat cat aat cat atg ggt gcc att gga gga ggt gga cct gta ggg 362  
Gly Asn His Asn His Met Gly Ala Ile Gly Gly Gly Gly Pro Val Gly  
60 65 70 75

ttt cat aat cag atg ttt ccg ttg gga tta agt ctc gat caa ggg aaa 410  
Phe His Asn Gln Met Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys  
80 85 90





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 ttttgttcaa agacttttagt gtgattttca ggaccaaggg ctttgaggggt agtgctagct 1323  
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                           35                          40                          45  
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           65                          70                          75                          80  
 Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys Gly His Gly Phe Leu  
                           85                          90                          95  
 Lys Pro Asp Glu Thr Gly Lys Arg Phe Gln Asp Asp Val Leu Asp Asn  
                           100                          105                          110  
 Arg Cys Ser Ser Met Lys Pro Ile Phe His Gly Gln Pro Met Ser Gln  
           115                          120                          125  
 Pro Ala Pro Pro Met Pro His Gln Gln Ser Thr Ile Arg Pro Arg Val  
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 Arg Ala Arg Arg Gly Gln Ala Thr Asp Pro His Ser Ile Ala Glu Arg  
           145                          150                          155                          160  
 Leu Arg Arg Glu Arg Ile Ala Glu Arg Ile Arg Ser Leu Gln Glu Leu  
                           165                          170                          175  
 Val Pro Thr Val Asn Lys Thr Asp Arg Ala Ala Met Ile Asp Glu Ile  
                           180                          185                          190  
 Val Asp Tyr Val Lys Phe Leu Arg Leu Gln Val Lys Val Leu Ser Met  
           195                          200                          205

CCF60:G79360



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ggc gga gga gga gga ggg tta aca gtg gga cac aca atg ggg act tcg 437  
 Gly Gly Gly Gly Gly Gly Gly Leu Thr Val Gly His Thr Met Gly Thr Ser  
                   125                  130                  135

tta atg ggt ggt ggt ggt tct ggt ggg ttt tgg gct gtt ccg gcg agg 485  
 Leu Met Gly Gly Gly Gly Ser Gly Gly Phe Trp Ala Val Pro Ala Arg  
                   140                  145                  150

ccg gat ttc gga caa gtc tgg agc ttt gca acc gga gct cca ccg gaa 533  
 Pro Asp Phe Gly Gln Val Trp Ser Phe Ala Thr Gly Ala Pro Pro Glu  
                   155                  160                  165

atg gtt ttt gcg cag cag cag caa cca gct aca ctc ttc gtc cgc cac 581  
 Met Val Phe Ala Gln Gln Gln Gln Pro Ala Thr Leu Phe Val Arg His  
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cag cag caa cag caa gct tcc gcc gcc gca gca gct gca atg ggt gag 629  
 Gln Gln Gln Gln Gln Ala Ser Ala Ala Ala Ala Ala Ala Met Gly Glu  
                   190                  195                  200

gct tca gca gct aga gtt ggg aat tat ctt ccg ggt cat cat ctc aat 677  
 Ala Ser Ala Ala Arg Val Gly Asn Tyr Leu Pro Gly His His Leu Asn  
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ttg ctt gct tct ttg tct ggt gga gct aac ggg tcg ggt cgg agg gaa 725  
 Leu Leu Ala Ser Leu Ser Gly Gly Ala Asn Gly Ser Gly Arg Arg Glu  
                   220                  225                  230

gac gac cac gaa cca cgt tgagaaatgg tattgtcttt ttggtaatgt 773  
 Asp Asp His Glu Pro Arg  
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atagaaaaat tcctatgttt tatgtcatcg aaagtgttta gaaagtacct ctaatttgcg 833

gtttcttttg ctcttttttt acttaattta agcttattgc ttgtttgatt agggtttttag 893

ggtttaagaa tatttggctct cgtaatttg tttcggagag tgatagaaag agagagagat 953

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66160-6154660



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Asn Asp Thr Ala Ala Val Ala Thr Gly Gly Gly Ala Arg Gln Leu Val	
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Asp Ala Ser Leu Ser Ile Val Pro Arg Ser Thr Pro Pro Glu Asp Ser	
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Thr Leu Ala Thr Thr Ser Ser Thr Ala Thr Ala Thr Thr Lys Arg	
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Ser Thr Lys Asp Arg His Thr Lys Val Asp Gly Arg Gly Arg Arg Ile	
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Arg Met Pro Ala Leu Cys Ala Ala Arg Val Phe Gln Leu Thr Arg Glu	
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Leu Gly His Lys Ser Asp Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln	
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gct gag cca gct att gtt gct gct aca ggt aca gga act att ccg gcg	508
Ala Glu Pro Ala Ile Val Ala Ala Thr Gly Thr Gly Thr Ile Pro Ala	
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aac ttc tct act tta agt gtt tcg tta cga agt agt gga tcg act ctc	556
Asn Phe Ser Thr Leu Ser Val Ser Leu Arg Ser Ser Gly Ser Thr Leu	
125 130 135	
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Ser Ala Pro Pro Ser Lys Ser Val Pro Leu Tyr Gly Ala Leu Gly Leu	
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act cat cat cag tat gat gaa caa gga ggc ggc ggt gtg ttt gct gct	652
Thr His His Gln Tyr Asp Glu Gln Gly Gly Gly Gly Val Phe Ala Ala	
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cat acg tcg ccg ctt tta ggg ttt cat cat cag ctt caa cac cac cag	700
His Thr Ser Pro Leu Leu Gly Phe His His Gln Leu Gln His His Gln	
175 180 185	
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Asn Gln Asn Gln Asn Gln Asp Pro Val Glu Thr Ile Pro Glu Gly Glu	
190 195 200	
aat ttc tct agg aaa cgg tat aga tcg gtt gat ttg tct aaa gaa aac	796
Asn Phe Ser Arg Lys Arg Tyr Arg Ser Val Asp Leu Ser Lys Glu Asn	
205 210 215	

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Asp Asp Arg Lys Gln Asn Glu Asn Lys Ser Leu Lys Glu Ser Glu Thr	
220 225 230	
tcg ggt cct acg gcg gcg ccg atg tgg gcg gtt gcg ccg ccg agt agg	892
Ser Gly Pro Thr Ala Ala Pro Met Trp Ala Val Ala Pro Pro Ser Arg	
235 240 245 250	
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Ser Gly Ala Gly Asn Thr Phe Trp Met Leu Pro Val Pro Thr Thr Ala	
255 260 265	
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Gly Asn Gln Met Glu Ser Ser Ser Asn Asn Asn Thr Ala Ala Gly His	
270 275 280	
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Arg Ala Pro Pro Met Trp Pro Phe Val Asn Ser Ala Gly Gly Gly Ala	
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Gly Gly Gly Gly Gly Ala Ala Thr His Phe Met Ala Gly Thr Gly Phe	
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Ser Phe Pro Met Asp Gln Tyr Arg Gly Ser Pro Leu Gln Leu Gly Ser	
315 320 325 330	
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Phe Leu Ala Gln Pro Gln Pro Thr Gln Asn Leu Gly Leu Ser Met Pro	
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Asp Ser Asn Leu Gly Met Leu Ala Ala Leu Asn Ser Ala Tyr Ser Arg	
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Gly Gly Asn Ala Asn Ala Asn Ala Glu Gln Ala Asn Asn Ala Val Glu	
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His Gln Glu Lys Gln Gln Gln Ser Asp His Asp Asp Asp Ser Arg Glu	
380 385 390	
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Glu Asn Ser Asn Ser Ser Glu	
395 400	
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Gly Glu Thr Ile Glu Trp Leu Leu Gln Gln Ala Glu Pro Ala Ile Val  
100 105 110

Val Ser Leu Arg Ser Ser Gly Ser Thr Leu Ser Ala Pro Pro Ser Lys  
130 135 140

Glu Gln Gly Gly Gly Gly Val Phe Ala Ala His Thr Ser Pro Leu Leu  
165 170 175

Gly Phe His His Gln Leu Gln His His Gln Asn Gln Asn Gln Asn Gln  
180 185 190

Asp Pro Val Glu Thr Ile Pro Glu Gly Glu Asn Phe Ser Arg Lys Arg  
195 200 205

Tyr Arg Ser Val Asp Leu Ser Lys Glu Asn Asp Asp Arg Lys Gln Asn  
210 215 220

Glu Asn Lys Ser Leu Lys Glu Ser Glu Thr Ser Gly Pro Thr Ala Ala  
225 230 235 240

Pro Met Trp Ala Val Ala Pro Pro Ser Arg Ser Gly Ala Gly Asn Thr  
245 250 255

Phe Trp Met Leu Pro Val Pro Thr Thr Ala Gly Asn Gln Met Glu Ser  
260 265 270



Ser Ser Asn Asn Asn Thr Ala Ala Gly His Arg Ala Pro Pro Met Trp  
 275 280 285

Pro Phe Val Asn Ser Ala Gly Gly Gly Ala Gly Gly Gly Gly Gly Ala  
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Ala Thr His Phe Met Ala Gly Thr Gly Phe Ser Phe Pro Met Asp Gln  
 305 310 315 320

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 325 330 335

Pro Thr Gln Asn Leu Gly Leu Ser Met Pro Asp Ser Asn Leu Gly Met  
 340 345 350

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 Val Thr Thr Pro Ala Pro Ala Asp Thr Pro Ala Pro Ala Pro Ala Glu  
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655150-615160

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 Phe Gln Trp Ile Gly Gly Phe Arg Pro Ser Glu Leu Leu Asn Val Val  
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 Met Pro Tyr Leu Gln Pro Leu Thr Asp Gln Gln Ile Leu Glu Val Arg  
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 325 330 335  
  
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&lt;211&gt; 368

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Lys	Ser	Asp	Ile	Asn	Asp	His	Ser	Pro	Asn	Thr	Ala	Thr	Ser	Ser	Ile
		35					40					45			
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His	Trp	Leu	Gln	Glu	Gln	Ser	Arg	Arg	Val	Ser	Glu	Leu	Arg	Thr	Ala
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gta gtg ggt cac cca ata cta gaa tca ggc ttg aac act tct tac cat 947  
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gac Asp 35	ccc Pro	aag Lys	cct Pro	cgc Arg	ctt Leu 40	cgt Arg	tgg Trp	acc Thr	tct Ser	gag Glu 45	ctc Leu	cat His	gaa Glu	aga Arg	ttc Phe 50	261
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Arg Phe Val Asp Ala Val Thr Gln Leu Gly Gly Pro Asp Lys Ala Thr  
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Pro Lys Thr Ile Met Arg Thr Met Gly Val Lys Gly Leu Thr Leu Tyr  
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His Leu Lys Ser His Leu Gln Lys Phe Arg Leu Gly Arg Gln Ser Cys  
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